

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 11:01:45 ; Search time 2991 Seconds

(without alignments)
8737.653 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898
Sequence: 1 ctcgcacgcactcgcacgcctc.....aaaaaaaaaaaaaaaaaaaaa 898

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hvg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
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26: em_ro:*
27: em_sts:*
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31: em_hvg_inv:*
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33: em_hvg_mus:*
34: em_hvg_pla:*
35: em_hvg_rod:*
36: em_hvg_mam:*
37: em_hvg_vrt:*
38: em_sv:*
39: em_hvg_hum:*
40: em_hvg_mus:*
41: em_hvg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329.4	36.7	144973	2 AC096689	AC096689 Oryza sat
2	329.4	36.7	150928	2 AC103550	AC103550 Oryza sat
3	171.6	19.1	110235	2 AP004057	AP004057 Oryza sat
4	171.6	19.1	153428	2 AP005535	AP005535 Oryza sat
5	140.6	15.7	716	8 ZMU82200	ZMU82200 Zea mays sat
6	134	14.9	155939	8 AP003853	AP003853 Oryza sat
7	129	14.4	110235	2 AP004057	AP004057 Oryza sat
8	121.8	13.6	153428	2 AP005535	AP005535 Oryza sat
9	117.4	13.1	151673	8 AC097278	AC097278 Oryza sat
10	113	12.6	864	8 AF306651	AF306651 Oryza sat
11	111	12.4	129918	8 OSJN00280	OSJN00280 Oryza sat
12	110.4	12.3	123272	2 AP005604	AP005604 Oryza sat
13	110.4	12.3	123272	2 AP005309	AP005309 Oryza sat
14	110.4	12.3	137275	2 AC128878	AC128878 Rattus no
15	104.8	11.7	172838	2 TAET7348	TAET7348 Trifolium
16	104	11.6	799	8 AF251277	AF251277 Oryza sat
17	103.6	11.5	813	8 OSA278436	OSA278436 Oryza sat
18	103.6	11.5	830	8 AP003754	AP003754 Oryza sat
19	101.6	11.3	129052	2 AP003754	AP003754 Oryza sat
20	101.2	11.3	734	8 HVPRIAR	HVPRIAR H. vulgare H
21	100.8	11.2	740	8 HVPRIAR	HVPRIAR H. vulgare H
22	99.4	11.1	582	8 TAET7349	TAET7349 Trifolium
23	98.4	11.0	129052	2 AP003754	AP003754 Oryza sat
24	97	10.8	784	8 ZMPRMS	ZMPRMS Zea mays sat
25	96.4	10.7	137275	2 AP005309	AP005309 Oryza sat
26	94.6	10.5	836	8 AF384143	AF384143 Trifolium
27	94.4	10.5	1444	8 HVPRIAR	HVPRIAR H. vulgare B
28	93.8	10.4	138467	2 AC111697	AC111697 Rattus no
29	93.6	10.4	719	8 HVPRIAR	HVPRIAR H. vulgare m
30	93.6	10.4	759	8 HVPRIAR	HVPRIAR H. vulgare m
31	93.6	10.4	1917	8 HVPRIAR	HVPRIAR H. vulgare H
32	93.4	10.4	2031	8 OSU89895	OSU89895 Oryza sat
33	93.4	10.4	155939	8 AP003853	AP003853 Oryza sat
34	92.2	10.3	874	8 SNPRJRE9	SNPRJRE9 Oryza sat
35	92.2	10.3	137785	2 AP005065	AP005065 Oryza sat
36	92.2	10.3	176171	2 AP005065	AP005065 Oryza sat
37	92	10.2	687	8 HVPRIAR	HVPRIAR H. vulgare m
38	91.4	10.2	108782	2 AC123508	AC123508 Rattus no
39	91	10.1	61958	2 AC121467	AC121467 Rattus no
40	90.6	10.1	62847	2 AC125560	AC125560 Rattus no
41	89.6	10.0	158897	2 AC121439	AC121439 Rattus no
42	89.6	10.0	191976	2 AC117044	AC117044 Rattus no
43	89	9.9	136788	2 AC117044	AC117044 Rattus no
44	88	9.8	159101	2 AC126205	AC126205 Rattus no
45	87.8	9.8	99329	2 AC099247	AC099247 Rattus no

ALIGNMENTS

RESULT 1
AC096689 144973 bp DNA linear HTG 09-JAN-2002
LOCUS Oryza sativa chromosome 3 clone OSJNB0027J18, *** SEQUENCING IN
ACCESSION AC096689
VERSION AC096689.3 GI:18092993
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 144973)
Buell,R., Hsiao,J., Zismann,V., Mofat,K.M., Hill,J.,


```

* 85050 95622: contig of 10573 bp in length
* 95623 95669: gap of unknown length
* 95670 109958: contig of 14289 bp in length
* 109959 110005: gap of unknown length
* 110006 124211: contig of 14206 bp in length
* 124212 124258: gap of unknown length
* 124259 131728: contig of 7470 bp in length
* 131729 131775: gap of unknown length
* 131776 133914: contig of 2139 bp in length
* 133915 133961: gap of unknown length
* 133962 141548: contig of 7587 bp in length
* 141549 141595: gap of unknown length
* 141596 144303: contig of 2708 bp in length
* 144304 144349: gap of unknown length
* 144350 148834: contig of 4485 bp in length
* 148835 148880: gap of unknown length
* 148881 150928: contig of 2048 bp in length.

FEATURES
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            /cultivar="Nipponbare"
            /db_xref="taxon:4530"
            /chromosome="3"
            /clone="OSJNBa0079612"
            /note="Japanese cultivar-group"
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ORIGIN
Query Match      36.7%; Score 329.4; DB 2: Length 150928;
Best Local Similarity 78.5%; Pred. No. 1,9e-32;
Matches 450; Conservative 0; Mismatches 106; Indels 17; Gaps 4;

QY 107 GGCATAGGCGACGGGCGTGTCTTCCTGCGCAACCCCTCTGCGTGTGCGCGCGCGCGCGCG
Db 68748 GCGGATGCGCGCGCGCTGCTGCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 167 GCGGACCCACG -GCGCGCGCGCTCTCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68691 GCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 226 AGCAGGTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68638 AGCAGGCGAAGCGCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 286 ACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68578 ACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 346 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68518 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 400 ACCTGGGGGCGACGCCCTCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68458 ACATGAGCGGAGCCCTCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 460 CCGAGGTGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db 68398 CCGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
QY 520 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68338 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 580 TCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68278 TCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 640 CGCAGCGCAAGTCGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTACT
Db 68218 CGCAGCGCAAGTCGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTACT

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RESULT 3
LOCUS AP004057/c 110235 bp DNA linear HTG 21-MAR-2002
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 2 clone
AP004057.1 GI:15208425
ACCESSION AP004057
VERSION 1
KEYWORDS HTG; PHASE2
SOURCE HTG; PHASE2
ORGANISM Oryza sativa (japonica cultivar-group) (cultivar: Nipponbare) DNA,
clone: OJ1316_E06.
REFERENCE 1
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
JOURNAL clone: OJ1316_E06
REFERENCE 2
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Published Only in Database (2001)
JOURNAL 2 (bases 1 to 110235)
Direct Submission
Submitted (15-AUG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
    source
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            /organism="Oryza sativa (japonica cultivar-group)"
            /cultivar="Nipponbare"
            /db_xref="taxon:3947"
            /chromosome="2"
            /clone="OJ1316_E06"
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ORIGIN
Query Match      19.1%; Score 171.6; DB 2: Length 110235;
Best Local Similarity 59.1%; Pred. No. 8e-13;
Matches 311; Conservative 0; Mismatches 214; Indels 1; Gaps 1;

QY 147 GCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76921 GCTCTAGGAGGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 207 GCGCGGTATCAAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG
Db 76861 CGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 267 GAGTACTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76802 CAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
QY 327 AACGCGGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76742 AGCAGGACACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 387 TCGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76682 GCGGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

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QY	447	CGGCGGCGCCGCGAGGTTGTGGCGCTGTGGGGGGGAGGGGGCGTACTACACCCAC	506
Db	76522	GCGTGGAGCGCCAGCCACCGGTGGCGGGGGTGGGGGGAGGGGGCGACCTACGACTAC	76563
QY	507	GCCACMACACGTTGCGCCGCGGGGGGGGAGAGTGTGGCGACGTACAGCAGAGTGTGGGCGC	566
Db	76562	GGCGCCACCGGTGGCGGGGGGGGAGAGTGTGGCGACGTACAGCAGAGTGTGGGCGC	76503
QY	567	AACACGCGCCGAGGTGCGGTTGCGCGCAGGCGCACTTGTGCGCACGGGCGCCAGCTACGCTTC	626
Db	76502	GACAGCAGCGAGGTGCGGCTGCGCCACCGCTACACTGTCTCTCCGCGGAGAGCTCATGGCG	76443
QY	627	TGCGGTACACACCGCAGCGCAAGTGCAGGGGCGAGAGCCCTACT	672
Db	76442	TGCGCACTACGAGCGCGAGGGCACAATCATGGGGCGAGAGCCCTTCT	76397

RESULT 4	AP005535/c	LOCUS	DEFINITION
AP005535	153428 bp	DNA	linear HTG 19-JUL-2002
Oryza sativa (Japonica cultivar-group)			chromosome 2 clone
OSJNBA0054A20, ***		SEQUENCING IN PROGRESS ***	in ordered pieces.
AP005535			
AP005535.1	GI:21908009		
HTG; HTGS-PHASE2.			
Oryza sativa (Japonica cultivar-group)			(cultivar:Nipponbare) DNA,

ORGANISM *Oryza sativa* (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzaceae, *Oryza*.

1
REFERENCE
AUTHORS
TITLE
Sasaki, T., Matsumoto, T. and Katayose, Y.
Oryza sativa nippohbare(GA3) genomic DNA, chromosome 2, BAC
clone: OJURBa0054K20
2
JOURNAL
REFERENCE
AUTHORS
TITLE
Published only in database (2002)
2 (bases 1 to 153428)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (18-JUL-2002) Takuji Sasaki, National Institute of

JOURNAL Submitted (18-JUL-2002) Takaji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL: <http://rgrp.dna.affrc.go.jp/>)
Tel:81-296-38-7441, Fax:81-296-38-7468

COMMENT Note: It currently consists of 1 contigs. Gaps between the contigs

COMMENT

NOTE: It currently consists of 1 control Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES	Location/Qualifiers
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	/cultivar="Nippohare"
	/db_xref="taxdb:39947"
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	/clone="OSUNBa0054K20"
BASE COUNT	43229 a 34064 c 34373 g 41801 t 61 others
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Query Match	19.1%;	Score 171.6;	DB 2;	Length 153428;
Best Local Similarity	59.1%;	Pred. No. 7.6e-13;		
Matches 311;	Conservative 0;	Mismatches 214;	Indels 1;	Gaps 1;

Db 21141 GCTCAGGAGGCTCTCCTGCTGCGTCCGCGCTGGCCGCGCTGCTGCTCCTGTGTCGCGCA 21082

207 GCGCGGTGACCAAGCGCAGCAGGGTGGCACC GCGCAGCGCAGCAACGCGACGGGAC 266

[illegible]

RESULT	5
Locus	ZMU82200
DEFINITION	ZMU82200 716 bp mRNA linear PLN 06-JUN-1998
ACCESSION	U82200
VERSION	082200.1 GI:3290003
KEYWORDS	.
SOURCE	Zea mays.
ORGANISM	Zea mays

REFERENCE
AUTHORS

1 (bases 1 to 716)

Morris, S.W., Vernooij, B., Titarov, S., Starrett, M., Thomas, S.,
Willsie, C.C., Frederiksen, R.A., Bhadnurfaick, A., Hulbert, S. and
Uknes, S.

TITLE	Induced resistance responses in maize
JOURNAL	Mol. Plant Microbe Interact. 11 (7), 643-658 (1998)
MEDLINE	98319983
PUBMED	9650297
REFERENCE	2 (bases 1 to 716)
AUTHORS	Morris, S.W., Vernooij, B., Hulbert, S., Starrett, M., Thomas, S. and Unke, S.
TITLE	Direct Submission
JOURNAL	Submitted (13-DEC-1996) Ciba-Geigy, P.O. Box 12257, Research Triangle Park, NC 27709-2257, USA
FEATURES	Location/Qualifiers

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QYDHDITNSCAEGQVCGHYTQVVRDSTAIGCARVCCDNNAGVFIICSYNPNPNNVGE

AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
 TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
 clone:OUJ316.E06
 JOURNAL Published Only in database (2001)
 REFERENCE 2 (bases 1 to 110235)
 AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
 JOURNAL Direct Submission
 Submitted (15-AUG-2001) Takuji Sasaki, National Institute of
 Agricultural Resources, Rice Genome Research Program, Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@nias.affrc.go.jp, URL:http://irp.dna.affrc.go.jp/
 Tel:81-298-38-7441, Fax:81-298-38-7468)
 The nucleotide sequence of this BAC clone was generated by
 combining Monsanto and RGP-Japan sequencing data.
 NOTE: It currently consists of 1 contigs. Gaps between the contigs
 are represented as runs of N. The order of the pieces is believed
 to be correct as given, however the sizes of the gaps between them
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 sequence will be replaced by the finished sequence as soon as it is
 available and the accession number will be preserved.
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES
 source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /chromosome="2"
 /clone="OUJ316.E06"

BASE COUNT 30404 a 23562 c 24043 g 32226 t
 ORIGIN

Query Match 14.4%; Score 129; DB 2; Length 110235;
 Best Local Similarity 54.0%; Pred. No. 1.5e-07;
 Matches 320; Conservative 0; Mismatches 255; Indels 18; Gaps 2;

OY 98 GCTCCCGCCGCCATGAGCGACGCGCTGCTCCTCGCCACCTCTCGCGCTCTGCGC 157
 DB 74910 GCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 74969
 OY 158 CG 217
 DB 74970 CG 75029
 OY 218 CAAGCG 277
 DB 75030 CATGTCGCTGCGCAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 75089
 OY 278 G-----CGGCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
 DB 75090 GTTCTCTACTACCACTAGTGTGCGGTGCGCGGTGCGGTGCGGTGCGGTGCGGTG 75149
 OY 329 CGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 388
 DB 75150 GCGCGCGCTGAGTGTGCTGAGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 75209
 OY 389 CGCGTTCGCGAGCG 439
 DB 75210 GCGCGACTGCTTCCGAGAGGCGAGTTCGCGCTCGGGGAGAAATCTTTTGGGCGGG 75269
 OY 440 GAGCTACCGCTA 499
 DB 75270 CGGGGGGCGTGGCTA 75329
 OY 500 CACCACGCGCAACAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 559
 DB 75330 CTGCTAGCGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 75389
 OY 560 GTGGCGCAACACCGCGCGAGGTGCGGTGCGCGAGCGCGCTGCGCGCGCGCGCGCG 619
 DB 75390 GTGGCGCGCAACCTCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 75449

OY 620 CAGCTCTGCTGTACACCGCGACGCGACGTCGAGGCGCGCGCTACT 672
 DB 75450 CATGACTGTGACTACTACCGCGCGGTGAGTGTGCGCGAGGCGCGTACT 75502

RESULT 8
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 LOCUS 153428 bp DNA linear HTG 19-JUL-2002
 DEFINITION Oryza sativa (japonica cultivar-group) chromosome 2 clone
 OSJNBa0054K20, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
 ACCESSION AP005535
 VERSION AP005535.1 GI:21908009
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
 clone:OSJNBa0054K20.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.
 TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
 clone:OSJNBa0054K20
 JOURNAL Published Only in database (2002)
 REFERENCE 2 (bases 1 to 153428)
 AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.
 JOURNAL Direct Submission
 Submitted (18-JUL-2002) Takuji Sasaki, National Institute of
 Agricultural Sciences, Rice Genome Research Program, Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@nias.affrc.go.jp, URL:http://irp.dna.affrc.go.jp/
 Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT
 NOTE: It currently consists of 1 contigs. Gaps between the contigs
 are represented as runs of N. The order of the pieces is believed
 to be correct as given, however the sizes of the gaps between them
 are based on estimates that have provided by the submitter. This
 sequence will be replaced by the finished sequence as soon as it is
 available and the accession number will be preserved.
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES
 source
 1..153428
 /organism="Oryza sativa (japonica cultivar-group)"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /chromosome="2"
 /clone="OSJNBa0054K20"

BASE COUNT 43229 a 34064 c 34273 g 41801 t 61 others
 ORIGIN

Query Match 13.6%; Score 121.8; DB 2; Length 153428;
 Best Local Similarity 54.3%; Pred. No. 1.2e-06;
 Matches 323; Conservative 0; Mismatches 252; Indels 20; Gaps 3;

OY 98 GCTCCCGCCGCCATGAGCGACGCGCTGCTCCTCGCCACCTCTCGCGCTCTGCGC 157
 DB 19128 GCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19187
 OY 158 CG 217
 DB 19188 CG 19247
 OY 218 CAAGCGCGAGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 277
 DB 19248 CATGTCGCTGCGCAAGTGGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 19307
 OY 278 G-----CGGCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
 DB 19308 GTTCTCTACTACCACTAGTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 19367

OY	329	CGGGGGCTGGCTTCGGGCGCGGGGACGTGGCGA---	CGAGGGGGGAGGAGGGG	385
Dp	19368	CCCCGGCTGGAATCTACGCCGGGTGTGGGGGGCCCA	CGCGCGCGGCGACTGGCCGC	19427
OY	386	GTCGGCTTCGGGACGTGGGGCCAGCCCTTACGGCGGA	-----ACAGGSGTGG	437
Dp	19428	TGGCGCACTGTTCGCCGGGGGGGAGTTTGGCTTC	GGGGGGAACATCTTCGGGGCGGG	19487
OY	438	GCGAGCTACCGCGCGCGCCCGCCGAGGTGGGGGCT	GTGGTGGTGGAGGGGCGGTAC	497
Dp	19488	GCGGGCGGCGCGTGGCGGCCCCCGGACCCCTCAAG	GAATGGCGCGCGGAGGGCGTGCAC	19547
OY	498	TACACCCAGCCACAAACACGTGCGCCGCGGGGGCG	AGTGGCGACGTACGCAAGTGTC	557
Dp	19548	TACTCTGACCGCCGCAACCGGTGCGCGCGGGCGG	CGGAGTGGCGGCACTACACCCGATGC	19607
OY	558	GTTGGGCGCAACACCCCGAGGTGGGTGGGTGGCG	AGGCAAGCACTCGCAAGGCGCGCATG	617
Dp	19608	GTTGGGGCGGCAACACCTCGGTGGGTGGCGCGCG	CGTCCGCTCTCGAAGAGGGCGGGCGTC	19667
OY	618	CTACAGCTTCGCTGTACAAACCCGCAAGCGCAACT	GTGCAAGGGCCAGAGCCCTCTACT	672
Dp	19668	TTATATGACTGTGACACTACTACCGCGGGGTACAT	GTGCGCGAGGAGCGGCTACT	19722

FEATURES

SOURCE

Genes were identified by a combination of several methods: Gene prediction programs including Pfennsch (<http://www.softberry.com/>), genscan and Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GenemarkHMM (Mark Borodovsky, <http://genemark.biology.gatech.edu/Genemark/>), and GeneSplicer (Mihaiela Pertea and Steven Salzberg, contact.mperita.lit.org) searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/vgl.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/xm/RepeatMasker.html>).

[illegible]

gene
mRNA
CDS

Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (<http://www.softberry.com/>), GenScan and Genesat+ (Chris Burge, <http://CCR-081.mlt.edu/GENSCAN.html>), GeneMarkEMM (Mark Borodovsky, <http://genemark.diclo.edu/genescan.edu/genemark/>), and GeneSplicer (Milhena Perita and Steven Salzberg, contact.mperita@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/vgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Rddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arlan Smil, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSJNB0038H12 (AC105932) and OSJNB0005F01 (AC104322).

Location/Qualifiers

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/map="R104305"

/clone="OSJNBa0040E17"

/note="japonica cultivar-group"

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KIDRPFREELXYSPPRADDHPHANYPEPLSLTPNLPPIHLKINPVLILN
IDPAGNSGRLVAFGRONTIDAELVIGAHGAKVFLPRLCPDSEDEPFRFR
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Db	458552 CCTGCGCCCGCTGCTCTGCGGTGGCATCTCGCTTGCCATTGGCGGCACACACACTTC 45793		
OY	248 CAGCAACGCGACGGCGGACGAGTACTTGGCCGCCACACACAGGAGCGCGAGGGGGTGG 307		
Db	45792 GGCGCAGAACACCGCGCACAGATAGTCAACCTCAACACAGCGCGCGGGCGGAGACGG 45733		
OY	308 CGTGGCCCGCGCTGCGGTGAACGCGGGCGCTTCCGGCGCCGCGGAGCGAGTGGCGCA 367		
Db	45732 CGTGGCGCGGTAAGTTGGGAGCCCAAGAGTGGCAGCTTGCGCGAAGAGTAGACGGGCCAA 45673		
OY	368 GCACGCGCGGCAAGCGGGGTGCGGCTTGGCGGACGTGGGGGCCACGCCCTACGGCGCAA 427		
Db	45672 GCGCGCGCGGATCGCGGCTGACACACTTCGCGGGCCCGCTAGCGCGAGAACAATCTT--- 45616		
OY	428 CCAAGGGGTGGCGAGCTACCGCGCGCGCCCGCCAGAGGTGTGAGCTGTGGTGCGGA 487		
Db	45615 CTGGGGCTCGGCGGGCGCGCGCTGGAGCGCGCGAGCGGAGTGGCTGTGGTGCGCA 45556		
OY	488 GGGGCGGTACTACACCACGCAACGACAGGTGGCGGGCGGGGGGAGGAGCGGCGACGTA 547		
Db	45555 GAAGAGACATACACTAGACAGACACACACTGTGGACCCCGGCAAGGTGTGGCGCACATA 45496		
OY	548 CACGCAAGTGTGTGGCGCAACCCCGGAGTGGGTGGCGGCGAGCGACCTGTGGCCAC 607		
Db	45495 CACCCAGAGTGTGTGGCGAAGTCCGTCCGATCGGTGGCGCGCGGTGTGTGGCGGCG 45436		
OY	608 G---GGCGCCACGCTACGCTGTGGCTGTACCAACCCGACGAGCAAGTGGAGGGCCAGAG 664		
Db	45435 GAACCGGGGGGTTCATCACTCACTCACTAGACCCCCCGGCAATTCAAGCGGCGAGGG 45376		
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DEFINITION	Oryza sativa pathogenesis-related protein 1 mRNA, complete cds.		
ACCESSION	AF306651		
VERSION	AF306651.1 GI:21304632		
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SOURCE	Oryza sativa.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarthralidae; Oryzaceae; Oryza.		
REFERENCE	Park,M.-Y., Moon,E. and Hwang,D.-J. Isolation and characterization of PRL from rice Unpublished		
AUTHORS	2. (bases 1 to 864) Park,M.-Y., Moon,E. and Hwang,D.-J.		
TITLE	Direct Submission		
REFERENCE	Submitted (19-SEP-2000) Molecular Genetics, National Institute of Agricultural Science and Technology, Seodunong, Suwon, Kyungki DO 441-707, Korea		
JOURNAL	Location/Qualifiers		


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RESULT 12
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DEFINITION Oryza sativa (japonica cultivar-group) chromosome 7 clone
OJ1212.C12, *** SEQUENCING IN PROGRESS ***; in ordered pieces.
ACCESSION AP005604
VERSION AP005604.1 GI:22091076
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:OJ1212.C12.
ORGANISM Oryza sativa (japonica cultivar-group) Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1212.C12
JOURNAL Published Only in Database (2002)
ACCESSION 2 (bases 1 to 123272)
VERSION AP005604.1 GI:22091076
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:OJ1212.C12.
ORGANISM Oryza sativa (japonica cultivar-group) Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1212.C12
JOURNAL Published Only in Database (2002)
ACCESSION 2 (bases 1 to 123272)
VERSION AP005604.1 GI:22091076
KEYWORDS HTG; HTGS_PHASE2.
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clone:OJ1212.C12.
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Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
COMMENT
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Best Local Similarity 56.6%; Pred. No. 3.1e-05;
Matches 248; Conservative 0; Mismatches 181; Indels 9; Gaps 2;
QY 251 CAACGCGAGCGGAGGAGTACCTGGCCCGCACACAGCGCGCGGTGGCGGT 310
DB 82504 CCGAGACGAGCGGAGGAGTACCTGGCCCGCACACAGCGCGCGGTGGCGGT 82563
QY 311 GGGCCCGCTGCGGTGAGACGCGCGGCTTGGCGCGCGGAGCGGCGGAGCA 370
DB 82564 CCGCGCGCTGCTGTGGGAGACACCTGCGCGCGGAGCGGAGCGGAGCA 82623
QY 371 GCGCGCGAGGCGGCTGCGGTGGCGAGCTGGGGGCCACCCCTACGCGCGACCA 430
DB 82624 CCGCGCGAGTGGCGGTGCGGTGGCGAGCTGGGGGCCACCCCTACGCGCGACCA 82683
QY 431 GGGGTGGCGAGCTACCGCGCGCGCGCGCGAGGTG-----GTGGCGGTGGGTGCG 484
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SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:OJ1212.C12.
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Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1212.C12
JOURNAL Published Only in Database (2002)
ACCESSION 2 (bases 1 to 123272)
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clone:OJ1212.C12.
ORGANISM Oryza sativa (japonica cultivar-group) Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
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JOURNAL Published Only in Database (2002)
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VERSION AP005604.1 GI:22091076
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Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
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The nucleotide sequence of this BAC clone was generated by
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NOTE: It currently consists of 1 contigs. Gaps between the contigs
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to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
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/chromosome="7"
/clone="OJ1212.C12"
BASE COUNT 32892 a 29747 c 29268 g 31115 t 250 others
ORIGIN
Query Match 12.3%; Score 110.4; DB 2; Length 123272;
Best Local Similarity 56.6%; Pred. No. 3.1e-05;
Matches 248; Conservative 0; Mismatches 181; Indels 9; Gaps 2;
QY 251 CAACGCGAGCGGAGGAGTACCTGGCCCGCACACAGCGCGCGGTGGCGGT 310
DB 28444 CCGAGACGAGCGGAGGAGTACCTGGCCCGCACACAGCGCGCGGTGGCGGT 28385
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Accession	Version	Keywords	Organism	Reference	Journal	Comment
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AUTHORS	1		<i>Oryza sativa</i> (japonica cultivar-group)	137275 bp		
TITLE	1		<i>Oryza sativa</i> (japonica cultivar-group)	137275 bp		
JOURNAL	1		<i>Oryza sativa</i> (japonica cultivar-group)	137275 bp		
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Best Local Similarity	56.6%	Pred. No. 3	1e-05	
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Db 120856	CCAACACACGCGCACCGACATCGTACACATCCACACGCGCCGCGGAGCGCCCTGGCT	120797		
OY 311	GGCCCGCTGGTGGTGGACGCGCGGCGCTGGCTTGGCGCGCGCGGAGCGAGTGGCGACGA	370		
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OY 371	CGCGCGCGCAGCGGGGTGGCGGCTTGGCGGAGCGTGGGGGCGCGCCCTACGCGCGCACCA	430		
Db 120736	CGCCGCGGACTGGCGGCTTGGCGGACATCCGATTCGACACACACTATCATGATCGCGACACT	120677		
OY 431	GGGTGGGCGAGCTACCGCGCGCGCCCGCGGAGTG-----GTGGCGCTTGGGTGGC	484		
Db 120676	GTCTGTGACACCCCTCCGTGCACAGCGTGGAGCGCGCGCAGGCTCGATCCACGAGGGTGGC	120617		
OY 485	GGAGGGGCGGTACTACACCCAGCCACAAACACGCGCGCGCGGCGGCGGACGCGGCGAC	544		
Db 120616	GGAGAGGGCTCTTACGACTACGACGACGACAGCGTGGCGCGCGCCATGTGGCGGCA	120557		
OY 545	GTACACGAGTGTGTGGCGACACCGCGGAGTGGGG---CGCGGACGCGACGCG	601		
Db 120556	CTACACGCAAGTGTGTGGCGGACACACCGCGGTGGAGTGGCGCGCTGCTGCTGCA	120497		
OY 602	CGCCACGCGGCGCACGCTCAGCGCTGTGCTGTACACCCGCGACGCGCAACGTCGAGGCCA	661		
Db 120496	CGCCACCGGAGGCGTCTTCTCATCTGCACCTACTTCCGCGCGACACGTCACAAACCA	120437		
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Db 120436	GAGCGCTACTACTAGCTAC	120419		
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LOCUS				
DEFINITION	Rattus norvegicus clone CH230-511P16, *** SEQUENCING IN PROGRESS			
ACCESSION	AC128878			
VERSION	AC128878.2			
KEYWORDS	HTG: HNGS.PHASE1.			
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
REFERENCE	1 (bases 1 to 172838)			
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,			
	Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,			
	Barbieri,J., Benton,J., Blmage,K., Blankenburg,K., Brando,D.,			
	Bouch,J., Bowie,S., Brievara,M., Brown,E., Brown,M., Bryant,N.P.,			
	Buay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,			
	Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,			
	Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,			
	Cleveland,C.D., Cox,C., Coyle,M.D., Dahmore,S.R., David,R.,			
	Devila,M.L., Davis,C., Davy-Carroli,L., Dedecine,D.A.,			
	Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,			
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	Earnhart,C., Edgar,D., Edwards,C.C., Elhai,C., Escotto,M.,			
	Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,			
	Gabisi,J., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,			
	Gorelli,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,			
	Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,			
	Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,			
	Homs,J.F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E.,			
	Jacobson,B., Jia,Y., Johnson,R., Jolivel,S., Joudan,S.,			
	Karlsson,E., Kelly,S., Khan,V., King,L., Korvah,J., Kovar,C.,			
	Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.,			
	Li,T., Li,Z., Lichtenarge,O., Lien,C., Liu,J., Liu,W., Lounseid,H.,			

Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Mathewar, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
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 Rivers, M., Rojas, A., Rojubokan, I., Rolfe, W., Ruiz, S., Savery, G.,
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 Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H.,
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 Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Umanai, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D.,
 Weltsch, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 172838)
 Worley, K.C.
 Direct Submission
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 172838)
 Worley, K.C.
 Direct Submission
 Submitted (02-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Aug 1, 2002 this sequence version replaced gi:21953102.

----- Genome Center -----
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information -----
 Center project name: KAXI
 Center clone name: CH230-51P16
 ----- Summary Statistics -----
 Sequencing vector: Plasmid:
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap, version 0.990329
 Consensus quality: 117283 bases at least Q40
 Consensus quality: 122934 bases at least Q30
 Consensus quality: 128074 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 55 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1127:	contig of 1127 bp in length
1128	1227:	gap of unknown length
1228	2910:	contig of 1683 bp in length
2911	3010:	gap of unknown length
3011	4361:	contig of 1351 bp in length
4362	4461:	gap of unknown length
4462	5971:	contig of 1510 bp in length
5972	6071:	gap of unknown length
6072	7285:	contig of 1214 bp in length
7285	7385:	gap of unknown length
7385	8693:	contig of 1308 bp in length
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8794	10216:	contig of 1423 bp in length
10217	10516:	gap of unknown length

10317 12126: contig of 1810 bp in length
 12127 12226: gap of unknown length
 12227 13410: contig of 1184 bp in length
 13411 13510: gap of unknown length
 13511 15382: contig of 1872 bp in length
 15383 15482: gap of unknown length
 15483 17296: contig of 1814 bp in length
 17297 17395: gap of unknown length
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 18902 19001: gap of unknown length
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 20177 20276: gap of unknown length
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 22706 22805: gap of unknown length
 22806 24404: contig of 1599 bp in length
 24405 24504: gap of unknown length
 24505 26132: contig of 1628 bp in length
 26133 28232: gap of unknown length
 28233 28257: contig of 2025 bp in length
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 28359 30252: contig of 1895 bp in length
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 39712 39811: gap of unknown length
 39812 42028: contig of 2217 bp in length
 42029 42128: gap of unknown length
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 74780 74882: gap of unknown length
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 78893 78992: gap of unknown length
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 83088 83187: gap of unknown length
 83188 87020: contig of 3833 bp in length
 87021 87120: gap of unknown length
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 95492 98921: contig of 3430 bp in length

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* 113545 113645: gap of unknown length
* 113645 117970: contig of 4325 bp in length
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* 122690 122791: gap of unknown length
* 122791 127623: contig of 4833 bp in length
* 127623 127724: gap of unknown length
* 127724 136739: contig of 9016 bp in length
* 136739 136840: gap of unknown length
* 136840 142131: contig of 5292 bp in length
* 142131 142232: gap of unknown length
* 142232 150986: contig of 8755 bp in length
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Query Match 11.7%; Score 104.8; DB 2; Length 172838;
Best Local Similarity 51.3%; Pred. No. 0.00015;
Matches 220; Conservative 0; Mismatches 209; Indels 0; Gaps 0;
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QY 102 CCCGCGCCATGCGCCACGCGCTGTCTCTCCGCACTCTCGCGCTGTGCGCGCG 161
Db 24026 CCGGCGCCCGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23967
QY 162 CCGGCGCCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 221
Db 23966 CCGGCGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23907
QY 222 GCGCAGCAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 281
Db 23906 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23847
QY 282 CACAMACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 341
Db 23846 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23787
QY 342 TCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 401
Db 23786 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23727
QY 402 GTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 461
Db 23726 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23667
QY 462 GAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 521
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QY 522 GCCGCGCGCG 530
Db 23606 GGGGAGGGG 23598
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Search completed: March 18, 2003, 15:14:28
Job time : 3824 secs
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:37 ; Search time 18 Seconds
(without alignments)
1084.183 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

Sequence: 1 MAHSRSHHLLLPAPMATA.....ATLTCLYNPHGNVQGSFY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357.5	32.9	214	2	S65052
2	331	30.5	163	2	T02054
3	318	29.3	140	2	A33155
4	308.5	28.4	164	2	S37166
5	307.5	28.3	172	2	T04990
6	304	28.0	167	2	S14969
7	304	28.0	168	2	B24620
8	304	28.0	184	2	S10205
9	302.5	27.9	179	2	S22531
10	297.5	27.4	163	2	T04989
11	296	27.3	168	2	C24620
12	294	27.1	166	2	S52627
13	290.5	26.8	164	2	S39474
14	288.5	26.6	164	2	T01693
15	288	26.5	161	2	T08154
16	288	26.5	162	2	D86143
17	288	26.5	168	2	A24620
18	286	26.4	168	2	S52626
19	285.5	26.3	164	2	T48294
20	285	26.3	205	2	T48294
21	284	26.2	168	2	T07330
22	283.5	26.1	167	2	S51679
23	281.5	25.9	159	2	S26238
24	277.5	25.6	159	1	VCT014
25	271	25.0	185	2	T10677
26	269	24.8	190	2	T04232
27	268.5	24.7	173	2	S47171
28	265.5	24.5	161	2	H84518
29	263.5	24.3	161	2	S65777

30	261.5	24.1	174	2	S71554	pathogenesis-relat
31	260.5	24.0	164	2	T04299	pathogenesis-relat
32	260	24.0	177	2	S04728	pathogenesis-relat
33	257.5	23.7	175	2	S43894	pathogenesis-relat
34	257	23.7	161	2	E85354	PR-1-like protein
35	256.5	23.6	210	2	T04233	pathogenesis-relat
36	249.5	23.0	161	2	T52399	pathogenesis-relat
37	246	22.7	176	2	F84583	pathogenesis-relat
38	243	22.4	161	2	B96537	pathogenesis-relat
39	242	22.3	168	2	T07146	hypothetical prote
40	242	22.3	177	2	T08126	pathogenesis-relat
41	234	21.6	162	2	A96537	pathogenesis-relat
42	197	18.2	160	2	D85077	hypothetical prote
43	191.5	17.6	177	2	D84583	probable pathogene
44	171.5	15.8	81	2	A05264	probable pathogene
45	167	15.4	204	2	S27448	Sc7 protein - bracc

ALIGNMENTS

RESULT 1

PISTILL-Specific protein stsl4 precursor - potato

C:Species: Solanum tuberosum (potato)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S65052

R:van Eldik, G.J.; Wingen, M.; Rulter, R.K.; van Herpen, M.M.A.; Schrauwen, J.A.M.; Plant Mol. Biol. 30, 171-176, 1996

A:Title: Molecular analysis of a pistill-specific gene expressed in the stigma and sty

A:Reference number: S65052; MID:96197407; PMID:8616234

A:Accession: S65052

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-214 <V>N>

A:Cross-references: EMBL:X82652; NID:g1236784; PIDN:CAA57976.1; PID:g1236785

C:Genetics:

A:Gene: stsl4

C:Superfamily: pathogenesis-related leaf protein

Query Match 32.9%; Score 357.5; DB 2; Length 214;
Best Local Similarity 41.3%; Pred. No. 7.8e-22;
Matches 76; Conservative 26; Mismatches 75; Indels 7; Gaps 3;

QY	22	LLIATLALCAAPRPHGARVLMPCAGAVTKAQQCGTSGSNATDEXLAPHNQAARAV	81
DB	36	LIFFQFLTLTASTLTHISAQTVPPPPPTSA-----ATPSRAQOEFLDAHNKARSEV	90
QY	82	GVAPLRMNAGLASAAAGTVAAQOROGCAFDVGAAPYGANGMASYR-ARPAEVALMV	140
DB	91	GVGPPLTMSPLAKETSLIVAYQDKONCSFANLSNKGQJMASGYVTPPMADSVW	150
QY	141	AESRYTYHANNTCACAGRCGTATQVWVRNTAEVGAQAQSCATG-ATLTCLYNPHGNVYG	199
DB	151	AEKFFYENNSCTGDCGCVYQIYWKKSIELGCAQPRCYBEPATLVTCFPPGNTVG	210
QY	200	OSPY 203	
DB	211	EKPY 214	

RESULT 2

T02054

pathogenesis related protein-1 - maize

C:Species: Zea mays (maize)

C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 11-May-2000

C:Accession: T02054

R:Morris, S.W.; Vernooij, B.; Titartarn, S.; Starrett, M.; Thomas, S.; Willse, C.C.; F

Mol. Plant Microbe Interact. 11, 643-658, 1998

A:Title: Induced resistance responses in maize.

A:Reference number: Z14524; MID:98513983; PMID:9650297

A:Accession: T02054

A>Status: preliminary; translated from GB/EMBL/DBJ

QY 162 YTOVWBRNTAEYGAQASCATGATITLCTLYNPHGNVQOSPY 203
| | | | | : : | | : | | : | | : | |
Db 120 YTOVWBRKSVRLGCAKVRONNGTIIISCNIDPRGNVYNEKPY 161

Search completed: March 19, 2003, 09:36:05
Job time : 19 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:38 ; Search time 11 Seconds
(without alignments)

765.427 Million cell updates/sec

Title: US-09-832-320-2

Sequence: 1 MAHSSHHHLLLPAPMATA.....ATLTLCLYNPHGVQGSQSPY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357.5	32.9	214	ST14_SOLITU	Q01495 solanum tub
2	304	28.0	167	PRMS_MATIZE	Q00008 zea mays (m
3	304	28.0	167	PR1B_TOBAC	P07053 nicotiana t
4	296	27.3	168	PR1C_TOBAC	P05042 nicotiana t
5	290.5	26.8	164	PR12_HORVU	P35792 hordeum vul
6	288.5	26.6	164	PR1_HORVU	P05968 hordeum vul
7	288	26.5	161	PR1_ARATH	P33154 arabidopsis
8	286	26.4	168	PR1A_TOBAC	P08299 nicotiana t
9	285.5	26.3	164	PR13_HORVU	P35793 hordeum vul
10	281.5	25.9	159	PR1_SAMNI	Q41359 sambucus ni
11	281.5	25.9	159	PR04_LYCES	Q04108 lycopersico
12	277.5	25.6	173	PR06_LYCES	P04284 lycopersico
13	268.5	24.7	173	PR1_MEDTR	Q40374 medicago tr
14	260	24.0	177	PR1A_TOBAC	P11670 nicotiana t
15	257.5	23.7	175	PR1A_LYCES	Q08697 lycopersico
16	167	13.4	204	SC7_SCHCO	P35794 schizophy11
17	166.5	15.3	214	SC14_SCHCO	P35795 schizophy11
18	163	15.0	881	YJH8_YEAST	P47033 saccharomyc
19	161	14.8	299	YJH9_YEAST	P47033 saccharomyc
20	129	11.9	329	YK23_YEAST	P36110 saccharomyc
21	127.5	11.8	206	VAS_VESVI	P35787 vespula vid
22	125.5	11.6	244	ABE1_MOUSE	Q05401 mus musculu
23	125.5	11.6	312	YR81_CAEEL	Q05566 caenorhabdi
24	124.5	11.5	234	VAS_SOLIN	P35785 vespula pen
25	123	11.3	204	VAS_VESPE	P35785 vespula fla
26	121	11.2	245	VAS_VESFL	P35785 vespula fla
27	120	11.1	204	CRS3_HORSE	Q10100 equus cabal
28	119.5	11.0	205	VAS_POLEX	P35759 polistes ex
29	118.5	10.9	203	VAS_POLAR	Q05108 dolichovesp
30	117.5	10.8	209	VAS_POLAN	Q05109 polistes an
31	117.5	10.7	424	ASF_ANCCA	Q16937 ancylostoma
32	116.5	10.7	215	VAS3_DOLMA	P10737 dolichovesp
33	116	10.7	242	HELO_HELHO	Q91055 heloderma h

34	115	10.6	202	1	VAS_VESMA	P81657 vespa manda
35	114.5	10.6	676	1	ICP0_HSVBU	P29188 bovine herp
36	113.5	10.5	246	1	ABG_RAT	P12020 rattus norv
37	113	10.4	204	1	VAS_VESGE	P35784 vespula ger
38	112	10.3	211	1	VAS_SOLRT	P35779 solenopsis
39	112	10.3	227	1	VAS_VESVO	Q05110 vespula vul
40	111	10.2	227	1	VAS52_DOLMA	P10736 dolichovesp
41	110.5	10.2	442	1	GAT4_HUMAN	P43694 homo sapien
42	110	10.1	183	1	CRVP_TRIMU	P79845 trimeresuru
43	110	10.1	204	1	VAS_VESMC	P35760 vespula mac
44	107.5	9.9	206	1	VAS5_POLDO	P81656 polistes do
45	105.5	9.7	205	1	VAS_VESSQ	P35786 vespula squ

ALIGNMENTS

RESULT 1	ST14_SOLITU	STANDARD:	PRT:	214 AA.
ID	ST14_SOLITU			
AC	Q01495;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	SRS14 protein precursor.			
GN	SRS14.			
OS	Solanum tuberosum (Potato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; easterids I; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=4113;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Datura; TISSUE=Pistil;			
RX	MEDLINE=96197407; PubMed=8616234;			
RA	van Eldik G.J., Wiggins M., Rutter R.K., van Herpen M.M.A.,			
RA	Schrauwen J.A.M., Willems G.J.;			
RT	"Molecular analysis of a pistil-specific gene expressed in the stigma			
RT	and cortex of Solanum tuberosum.";			
RL	Plant Mol. Biol. 30:171-176(1996).			
CC	- FUNCTION: MAY PROTECT THE OUTER TISSUES OF THE PISTIL FROM			
CC	PATHOGEN ATTACK.			
CC	- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE STIGMA AND STYLAR			
CC	CORTEX THROUGHOUT PISTIL DEVELOPMENT. NOT EXPRESSED IN OTHER			
CC	ORGANS.			
CC	- DEVELOPMENTAL STAGE: ACCUMULATES IN THE PISTIL AROUND 120 HOURS			
CC	BEFORE ANTHESIS AND INCREASES TOWARDS THE END OF FLOWER			
CC	DEVELOPMENT, WITH A MAXIMUM AT ANTHESIS.			
CC	- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;			
CC	INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.			
CC	-----			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION			
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CC	OR SEND AN EMAIL TO license@sib-sib.ch).			
CC	-----			
CC	EMBL: X82652; CAA57976.1; -.			
CC	HSSP: P04284; 1CFE.			
CC	InterPro: IPR001283; Allrgn_V5/TPX1.			
CC	Pfam: PF00188; SCP_1.			
CC	ProDom: PD000542; Allrgn_V5/TPX1; 1.			
CC	SMART: SM00198; SCP_1.			
CC	PROSITE: PS01009; SCP_AGS_PRL_SCP_1; FALSE_NEG.			
CC	PROSITE: PS01010; SCP_AGS_PRL_SCP_2; FALSE_NEG.			
CC	Repeat: Signal.			
CC	FT SIGNAL	1	19	POTENTIAL.
CC	FT CHAIN	20	214	SRS14 PROTEIN.
CC	FT REPEAT	13	19	3.5 X 2 AA TANDEM REPEAT OF Y-I.
CC	FT DOMAIN	59	65	POLY-PRO.
CC	SEQUENCE	214 AA;	23887 MW;	6CC7919DE2C3C2EF CRC64;

Db 89 WSGSDFLTAKAVEMVNEKORYADNSMTCAGOVCGHYTQVWVRNSVRCARVOCNNC 148

QY 184 ATLTLCLYNPHGVGQSPY 203

Db 149 GYIVSCNYPDPGNVIGKSPY 168

RESULT 5

PR12_HORVU ID PR12_HORVU STANDARD: PRT: 164 AA.

AC P35752; 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

OS Pathogenesis-related protein PR1-2 precursor.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Trilicaceae; Hordeum.

NCBI_TaxID=4513;

SEQUENCE FROM N.A.

RC STRAIN=CV. PSAKNON RESISTANT; TISSUE=Leaf;

RX MEDLINE=95036024; PubMed=7524728;

RA Mouradov A., Mouradova E., Scott K.J.;

RT "gene family encoding basic pathogenesis-related 1 proteins in

barley.";

PL Plant Mol. Biol. 26:503-507(1994).

CC - FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

CC AGAINST PATHOGENS.

CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

QY 142 EGRYTHANNTCAAGRCGCTGYQVWVRNABVCGMAQSCAT--GATLTLCLYNPHGVG 199

Db 102 EKKYNTGSMTCAGKVCCHYTQVWRASSTIGCARVCCNNRGVFT-CNTEPRNGIVS 160

QY 200 QSPY 203

Db 161 QKPY 164

RESULT 6

PR1_HORVU ID PR1_HORVU STANDARD: PRT: 164 AA.

AC 005968; 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

OS Pathogenesis-related protein 1 precursor.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Trilicaceae; Hordeum.

NCBI_TaxID=4513;

SEQUENCE FROM N.A.

RX MEDLINE=94033324; PubMed=8219079;

RA Mouradov A., Petrasovits L., Davidson A., Scott K.J.;

RT "A cDNA clone for a pathogenesis-related protein 1 from barley.";

PL Plant Mol. Biol. 23:439-442(1993).

CC - FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

CC AGAINST PATHOGENS.

CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

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OY 142 EGRYTHANNTCAGRCGCTGYOVWNRANTAEVGAQASCAT--GATLTCLCYNPHGNVG 199
DB 102 EKDIYGSNTCAAGKVCYGHYOVWNRASITGCAVCCNNRGVFTI-CNTEPRGNITG 160
OY 200 QSPY 203
DB 161 QKPY 164

RESULT 7
PRL_ARATH STANDARD; PRT: 161 AA.
ID PRL_ARATH
AC P33154;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1 precursor (PR-1).
GN AtPG14610 OR T6B13.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv Landsberg erecta; TISSUE=leaf;
RX MEDLINE=93005717; PubMed=1392369;
RA Uknes S., Mauch-Mani B., Moyer M., Potter S., Williams S.,
RA Duncher S., Chandler D., Slusarenko A., Ward E., Ryals J.,
RT "Acquired resistance in Arabidopsis.";
RL Plant Cell 4:645-656(1992).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=cv Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Beutis M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.B., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Crasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernm W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -1- FUNCTION: PARTIALLY RESPONSIBLE FOR ACQUIRED PATHOGEN RESISTANCE.
CC -1- SUBCELLULAR LOCATION: ACCUMULATES IN THE APOPLAST BEFORE
CC SECRETION.
CC -1- INDUCTION: INDUCED BY 2,6-DICHLOROISONICOTINIC ACID (INA) AND
CC SALICYLIC ACID (POSSIBLY AN ENDOGENOUS SIGNAL FOR ACQUIRED
CC RESISTANCE). STRONGLY INDUCED BY PATHOGEN INFECTION.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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DR EMBL: M90508; AAA32863.1; -
DR EMBL: AC005398; AAC69381.1; -
DR PIR: J01693; J01693.
DR HSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP_1.
DR PRINTS: PR00837; VSTPYLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPX1; 1.
DR SMART: SM00198; SCP; 1.

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DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
KW Plant defense; Signal; Pathogenesis-related protein.
FT SIGNAL 1 26
FT CHAIN 27 161
FT MOD_RES 27 27
FT DISULFID 70 138
FT DISULFID 113 117
FT DISULFID 133 147
FT SEQUENCE 161 AA; 17677 MW; 898B0F6547C3F84 CRC64;
SQ
Query Match 26.5%; Score 288; DB 1; Length 161;
Best Local Similarity 39.5%; Pred. No. 3.9e-16;
Matches 64; Conservative 19; Mismatches 65; Indels 14; Gaps 5;

OY 42 VLMPGAGAVYKAOOGSGSGSNRTADEYLAIPNORAAYGAPLRMNAGLASAAAGTVA 101
DB 14 VALGALVLPKAD-----SPDYLRVHNOARGAVGVGPQWDERVA-AIARSYA 63
OY 102 QORROGCAFADVAGSPYGANOGWASYRARPAEVALMWAEGRYYTHANNTCAGRCGCT 161
DB 64 EQLR-GNCRLLHSG-GPYGENTLAWGSDLSGVSANVMWYSEKANYNYAANTC--NGVCGH 119
OY 162 YTOVWNRANTAEVGAQASCATGATLTCLCYNPHGNVGQSPY 203
DB 120 YTOVWNRASVRLGCAKVCYKNNGGTILISCNIDPRGNVYNEKPY 161

RESULT 8
PRLA_TOBAC STANDARD; PRT: 168 AA.
ID PRLA_TOBAC
AC P08299;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1A precursor (PR-1A).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv Samsun NN;
RX MEDLINE=88015528; PubMed=3658669;
RA Cornelissen B.J.C., Horowitz J., van Kan J.A.L., Goldberg R.B.,
RA Bol J.F.;
RT "Structure of tobacco genes encoding pathogenesis-related proteins
RT from the PR-1 group.";
RL Nucleic Acids Res. 15:6799-6811(1987).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=cv Samsun NN;
RX MEDLINE=88083595; PubMed=3691804;
RA Ohsishi M., Matsunaka M., Yamamoto N., Tanaka Y., Kano-Murakami Y.,
RA Ozei Y., Kato A., Harada N., Ohsishi Y.;
RT "Nucleotide sequence of the PR-1 gene of Nicotiana tabacum.";
RL PDB Lett. 225:243-246(1987).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=cv Wisconsin 38;
RX Pfizner U.M., Pfizner A.J.P., Goodman H.M.;
RT "DNA sequence analysis of a PR-1a gene from tobacco: molecular
RT relationship of heat shock and pathogen responses in plants.";
RL Mol. Gen. Genet. 211:290-295(1988).
[4]
RN SEQUENCE OF 4-168 FROM N.A.
RP STRAIN=cv Xanthi;
RX MEDLINE=89041576; PubMed=3186451;
RT Cut J.R., Dixon D.D., Carr J.P., Kleissig D.F.;
RT "Isolation and nucleotide sequence of cDNA clones for the
RT pathogenesis-related proteins PRLa, PRLb and PRLc of Nicotiana

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RT tabacum cv. Xanthi nc induced by TMV infection."
RL Nucleic Acids Res. 16:9861-9861(1988).
RN [5]
RP SEQUENCE OF 30-70, 103-131 AND 157-168.
RA Lucas J., Camacho Henriquez A., Lottspeich F., Henschen A.,
RA Sanger H.L.
RT "Amino acid sequence of the 'pathogenesis-related' leaf protein p14
RT from virulent-infected tomato reveals a new type of structurally
RT unfamiliar proteins."
RL EMBO J. 4:2745-2749(1985).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE-91224081; PubMed-2026137.
RA Dixon J.C., Cutt J.R., Klessig D.F.
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts."
RL EMBO J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PTM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL; X05959; CAA29392.1; -.
DR EMBL; X06361; CAA29660.1; -.
DR EMBL; X12485; CAA31008.1; -.
DR EMBL; X06930; CAA30017.1; -.
DR PIR; S00513; S00513.
DR PIR; A05264; A05264.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1IKE.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 30
FT CHAIN 1 168
FT CONFLICT 5 6 LE -> VS (IN REF. 4).
FT CONFLICT 57 57 D -> S (IN REF. 5).
FT CONFLICT 68 69 SO -> PS (IN REF. 5).
FT CONFLICT 106 106 D -> N (IN REF. 3).
FT CONFLICT 153 153 S -> T (IN REF. 3).
FT CONFLICT 162 162 Y -> W (IN REF. 5).
SQ SEQUENCE 168 AA; 18573 MW; 2737521703129280 CRC64;
Query Match 26.4%; Score 286; DB 1; Length 168;
Best local Similarity 36.7%; Pred. No. 5; Ee -16;
Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;
OY 22 LLATLALCAAPAPTHGRVMPGAGAVTKAQQGGSSNATADEYLAIPNORAAV 81
DB 13 LTVSTLLFLVY---SHSCR-----AQNQQ-----DYDAINTARADV 48
OY 82 GVALPLRWNAAGLSAAAGTAAQOROGGCAFDVGA---SPYGAN--QGWAASRAPAEV 135
DB 49 GVEPLTWDDQVAAYAAQNTASQ-----LAADCNLVSHQGYGNLAEGSGDEMT-AAKA 100

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OY 136 VALMAEGRYTHANNTCAAGRCQGYTVQVWRNTAEYCAQASCATATLTCLYNPG 195
DB 101 VEMWVDEKQYDHDNSTCAQGVGCHTYQVWRNSRVRGARVCNNGVVCNTDPG 160
OY 196 NVQGSPEY 203
DB 161 NRGESPEY 168
RESULT 9
PRL3_HORVU
ID PRL3_HORVU STANDARD; PRT; 164 AA.
AC P37933;
DT 01-JUN-1994 (rel. 29, Created)
DT 01-JUN-1994 (rel. 29, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Pathogenesis-related protein PRL3-3 precursor (PR-1b) (HV-8).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Pskakon resistant, and cv. NK1558; TISSUE=leaf;
RX MEDLINE-95036024; PubMed-7524728;
RA Mouradov A., Mouradova E., Scott K.J.
RT "Gene family encoding basic pathogenesis-related 1 proteins in
RT barley."
RL Plant Mol. Biol. 26:503-507(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Pallas; TISSUE=leaf;
RX MEDLINE-94281675; PubMed-8012045;
RA Brynjelsson T., Sommer Knudsen J., Gregersen P.L., Collinge D.B.,
RA Ek B., Thordar-Christensen H.
RT "Purification, characterization, and molecular cloning of basic PR-1-
RT type pathogenesis-related proteins from barley."
RL Mol. Plant Microbe Interact. 7:267-275(1994).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z26321; CAA81230.1; -.
DR EMBL; Z26333; CAA81234.1; -.
DR EMBL; X74940; CAA52894.1; -.
DR PIR; S37189; S37189.
DR PIR; S37209; S37209.
DR PIR; S37167; S37167.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1IKE.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Plant defense; Pathogenesis-related protein; Signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 1 164
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID
FT DISULFID 68 140
FT 113 119 BY SIMILARITY.

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FT DISULFID 109 115 BY SIMILARITY.
FT DISULFID 131 145 BY SIMILARITY.
SQ SEQUENCE 159 AA; 17438 MW; A315B1DB6C0C826A CRC64;

Query Match 25.9%; Score 281.5; DB 1; Length 159;
Best Local Similarity 44.5%; Pred. No. 1,2e-15;
Matches 61; Conservative 13; Mismatches 54; Indels 9; Gaps 4;

OY 69 EYLAPHNORAAVGAPELRMNGLASAAGTVAQOROGCGCAFADVGASPYGAN--OGMA 126
Dy :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 DYLAHVNDARAQYGVGPMGDANLMSRAQNYA--NSRAGDCNLHSGA---GEMLAGGG 84

OY 127 SYRRAPEAVVALWVAEGRYTHANNNTCAAGROCGTGYOVWRNTAEVGAQASCATATL 186
Dy :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 DFTGRAA--VOLWVSERPDYNTATNQCVGKMKGHYTYVWRNSVRLGCGRARCNGMWF 142

OY 187 TLTLYNPHGNGVQGSYP 203
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 ISCNYPDVGNWVGRRPY 159

RESULT 12
PROG_LYCSES STANDARD; PRT; 159 AA.
AC P04284; 004109;
AD 20-MAR-1987 (Rel. 04, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related leaf protein 6 precursor (P6) (Ethylene-induced
DE protein P1) (P14) (PR protein).
GN PRL1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
ON NCBI_TaxID=4081;
RX MEDLINE=93043041; PubMed=1421154;
RA van den Berg-Velthuis G.C.M., de Wit P.J.G.M., Wagmakers C.A.M.,
RA "differential accumulation of mRNAs encoding extracellular and
RT intracellular PR proteins in tomato induced by virulent and avirulent
RT races of Cladosporium fulvum."
RL Plant Mol. Biol. 20:513-527(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. MILL; TISSUE=leaf;
RX MEDLINE=94151430; PubMed=8108502;
RA Tornero P., Rodrigo T., Conejero V., Vera P.;
RT "Nucleotide sequence of a cDNA encoding a pathogenesis-related
RT protein, pi-p14, from tomato (Lycopersicon esculentum).";
RL Plant Physiol. 102:325-325(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFN8; TISSUE=leaf;
RX MEDLINE=97348583; PubMed=9204567;
RA Tornero P., Gadea J., Conejero V., Vera P.;
RT "Two PR-1 genes from tomato are differentially regulated and reveal a
RT novel mode of expression for a pathogenesis-related gene during the
RT hypersensitive response and development.";
RL Mol. Plant Microbe Interact. 10:624-634(1997).
RN [4]
RP SEQUENCE OF 25-159;
RC STRAIN=cv. Rutgers;
RA Lucas J., Camacho Henriquez A., Lottspeich F., Henschen A.,
RA Sanger H.L.;
RT "Amino acid sequence of the 'pathogenesis-related' leaf protein P14
RT from viroid-infected tomato reveals a new type of structurally
RT unfamiliar proteins.";
RL EMBO J. 4:2745-2749(1985).
RN [5]

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RP STRUCTURE BY NMR.
RX MEDLINE=97220236; PubMed=9067611;
RA Fernandez C., Szyperski T., Bruyere T., Ramage P., Moesinger E.,
RA Wietlich K.;
RT "NMR solution structure of the pathogenesis-related protein P14a.";
RL J. Mol. Biol. 266:576-593(1997).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS. HAS ANTIFUNGAL ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION FOUND DURING DAYS 4 TO 8
CC AND DAYS 8 TO 12 AFTER INOCULATION WITH AN AVIRULENT AND A
CC VIRULENT PATHOGEN RESPECTIVELY.
CC INDUCTION: UPON INFECTION BY VIRULENT AND AVIRULENT RACES OF
CC PATHOGENS, FOR EXAMPLE FUNGAL PATHOGEN C. FULVUM. ALSO INDUCED BY
CC ETHYLENE.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL; M69248; AAA03616.1; -
DR EMBL; X68738; CAA48672.1; -
DR EMBL; Y08804; CAA70042.1; -
DR PIR; A03379; VCT014.
DR PIR; S26239; S26239.
DR PIR; S29628; S29628.
DR PDB; 1CFE; 12-NOV-97.
DR InterPro; IPR001283; Allrgn_v5/Tpx1.
DR Pfam; PF00188; SCP_1.
DR PRINTS; PR00837; V57PXLKE.
DR PRODOM; PD000542; Allrgn_v5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Plant defense; Pathogenesis-related protein; signal; Multigene family;
KW Fungicide; 3d-structure.
FT SIGNAL 1 24
FT CHAIN 25 159 PATHOGENESIS-RELATED LEAF PROTEIN 6.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 68 136
FT DISULFID 109 115
FT DISULFID 131 145
FT CONFLICT 123 127
SQ SEQUENCE 159 AA; 17520 MW; EA35AC3AC0DF3F4 CRC64;

Query Match 25.6%; Score 277.5; DB 1; Length 159;
Best Local Similarity 44.5%; Pred. No. 2,6e-15;
Matches 61; Conservative 13; Mismatches 54; Indels 9; Gaps 4;

OY 69 EYLAPHNORAAVGAPELRMNGLASAAGTVAQOROGCGCAFADVGASPYGAN--OGMA 126
Dy :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 DYLAHVNDARAQYGVGPMGDANLMSRAQNYA--NSRAGDCNLHSGA---GEMLAGGG 84

OY 127 SYRRAPEAVVALWVAEGRYTHANNNTCAAGROCGTGYOVWRNTAEVGAQASCATATL 186
Dy :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 DFTGRAA--VOLWVSERPDYNTATNQCVGKMKGHYTYVWRNSVRLGCGRARCNGMWF 142

OY 187 TLTLYNPHGNGVQGSYP 203
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 ISCNYPDVGNWVGRRPY 159

RESULT 13
PRL_MEDTR STANDARD; PRT; 173 AA.
AC Q40374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein PR-1 precursor.
GN PR-1.
OS Medicago truncatula (barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root.
RA MEDLINE=95175606; PubMed=7870819;
RA Szydlak-Strozycka U., Lescure N., Cullimore J.V., Gamas P.;
RA "A cDNA encoding a PR-1-like protein in the model legume Medicago
RT truncatula."
RT Plant Physiol. 107:273-274(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: X79778; CAA56174.1; -
DR HSSP: P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/7px1.
DR Pfam: PF00188; SCP. 1
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/7px1; 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP_AGS_PRI_SCP_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SCP_2; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 1 23 PATHOGENESIS-RELATED PROTEIN PR-1.
FT DISULFID 78 149 BY SIMILARITY.
FT DISULFID 122 128 BY SIMILARITY.
FT DISULFID 144 159 BY SIMILARITY.
SQ SEQUENCE 173 AA; 19760 MW; 898B00C9CD72DE4A CRC64;

Query Match 24.7%; Score 268.5; DB 1; Length 173;
Best Local Similarity 42.0%; Pred. No. 1.4e-14;
Matches 60; Conservative 19; Mismatches 59; Indels 5; Gaps 5;

QY 63 SNATADBYLAPHNOARAAGVAPLRNNAAGTAAAGTAAQRRGGCAEFADVASPYGAN 122
DB 34 SRSEFNOFLPONTARAAGVIRPLVMDKLTHTAQ-WYANORR-MDCAL-EHSNPPYEN 90
QY 123 OGMA5-YRAREAVVALVMAEGRYTHANTCAAGRCGCTYQVWRNTAEVGCAGQASC 181
DB 91 IFMGSGVMNNAQAVASAWDEKOFYNTWNSVCVDGEMCHTYQVWVGSTTKGACASVCS 150
QY 182 TG-ATLTLCLYNPHGNVQGSPPY 203
DB 151 DDKGTFMTCNYDPGPNYNGERP 173

RESULT 14
PR1A_TOBAC STANDARD; PRT; 177 AA.
AC P11670.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Basic form of pathogenesis-related protein 1 precursor (PRP 1).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi;
RA Payne G., Middlesteadt W., Desai N., Williams S., Dincher S.,
RA Carnes M., Ryals J.;
RA "Isolation and sequence of a genomic clone encoding the basic form of
RT pathogenesis related protein 1 from Nicotiana tabacum."
RT Plant Mol. Biol. 12:595-596(1989).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- PTM: TWO DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X14065; CAA32228.1; -
DR PIR: S04728; S04728.
DR HSSP: P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/7px1.
DR Pfam: PF00188; SCP. 1
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/7px1; 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP_AGS_PRI_SCP_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SCP_2; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 177 BASIC FORM OF PATHOGENESIS-RELATED
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID
FT FT (BY SIMILARITY).
SQ SEQUENCE 177 AA; 19729 MW; 3DA58AFB4C206E9 CRC64;

Query Match 24.0%; Score 260; DB 1; Length 177;
Best Local Similarity 39.9%; Pred. No. 6.7e-14;
Matches 57; Conservative 17; Mismatches 65; Indels 4; Gaps 3;

QY 61 SSNATADBYLAPHNOARAAGVAPLRNNAAGTAAAGTAAQRRGGCAEFADVASPYG 120
DB 21 SKAONSPODYLPNHAARROYGVGPMTDNRNLAAYKONVANO-RIGDGMTH-SHGPG 77
QY 121 ANOGASVYRAREAVVALVMAEGRYTHANTCAAGRCGCTYQVWRNTAEVGCAGQASC 180
DB 78 ENLAAPQOLNAGAAGVKKMWDEKRFYDYNNSCVG-VGCHTYQVWRNSVRLGCAVRAS 136
QY 181 ATGATLTLCLYNPHGNVQGSPPY 203
DB 137 NNGWEFTTCNYDPGPNYNGERP 159

RESULT 15
PR1A_LYCES STANDARD; PRT; 175 AA.
AC O08637.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1A1 precursor (PR-1A1).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;

```


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OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:38 ; Search time 30 Seconds
(without alignments)
1394.252 Million cell updates/sec

Title: US-09-832-320-2
Perfect score: 1085
Sequence: 1 MAHSRSHHDLPLPAPMATA.....ATLTCLYNPHGNVGQSPY 203

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organellar:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	348.5	32.1	185	10	09FY11 arabidopsis
2	331	30.5	163	10	082086 zea mays (m
3	325.5	30.0	191	10	092NX5 arabidopsis
4	313.5	28.9	164	10	09XN05 arabidopsis
5	309	28.5	167	10	08W084 oryza sativ
6	308.5	28.4	164	10	043489 hordeum vul
7	307.5	28.3	172	10	081889 arabidopsis
8	304	28.0	164	10	040597 arabidopsis
9	303.5	28.0	169	10	039188 arabidopsis
10	302.5	27.9	179	10	004106 arabidopsis
11	297.5	27.4	163	10	081888 arabidopsis
12	296.5	27.3	164	10	082714 triticum ae
13	294	27.1	166	10	039187 arabidopsis
14	293.5	27.1	164	10	094F73 arabidopsis
15	291.5	26.9	140	10	08S3W2 cucumis sat
16	288.5	26.6	159	10	0941G6 solanum tub

17	288	26.5	162	10	096344 brassica na
18	288	26.5	159	10	09LNU2 arabidopsis
19	287.5	26.5	153	10	09SCJ5 solanum tub
20	285	26.3	205	10	09L212 arabidopsis
21	284	26.2	168	10	09FE57 oryza sativ
22	284	26.2	179	10	09AT44 capsicum an
23	283	26.1	168	10	040557 arabidopsis
24	281	25.9	168	10	040397 arabidopsis
25	275.5	25.4	185	10	08W3X9 solanum tor
26	271	25.0	168	10	09SV22 arabidopsis
27	269.5	24.8	207	10	09FKL1 arabidopsis
28	269	24.8	190	10	09SW05 arabidopsis
29	265.5	24.5	161	10	09ZNS4 arabidopsis
30	264.5	24.4	173	10	082715 triticum ae
31	263.5	24.3	161	10	043392 brassica na
32	261.5	24.1	174	10	040035 hordeum vul
33	260.5	24.0	164	10	004000 oryza sativ
34	260.5	24.0	186	10	09SF44 arabidopsis
35	259.5	23.9	160	10	024026 lycopersico
36	257	23.7	161	10	09MOC8 arabidopsis
37	256.5	23.6	210	10	09SW04 arabidopsis
38	253.5	23.4	142	10	09LJL4 pyrus pyrif
39	249.5	23.0	161	10	09LJMS arabidopsis
40	246	22.7	176	10	039186 arabidopsis
41	243	22.4	161	10	09LPM7 arabidopsis
42	242.5	22.4	120	10	09LJL5 pyrus pyrif
43	242	22.3	168	10	024025 lycopersico
44	242	22.3	177	10	065157 capsicum an
45	234	21.6	162	10	09LPM6 arabidopsis

ALIGNMENTS

RESULT 1
Q9FY11 PRELIMINARY; PRT; 185 AA.
ID Q9FY11
AC Q9FY11:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similarity to pathogenesis-related protein (unknown protein)
DE (Hypothetical 20.1 kDa protein).
GN KLF13.27 OR AFS66590.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Physically assigned PI and TAC clones.";
RT DNA Res. 5:203-216(1998).
RL [2]
RN SEQUENCE FROM N.A.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

RA Kim C., Jin J., Liu S.-X., Narsaka M., Pham P.-K., Sekano H.,
RA Sakuai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Becker J., Theologis A., Davis R.W.,
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
RL EMBL: AB013389, BAB10935.1; -
DR EMBL: AF386987, AAK62432.1; -
DR EMBL: AY093248, AAM13247.1; -
DR HSSP: P04284; 1CPE.
DR InterPro: IPR001283, Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
KW Hypothetical protein
SQ SOURCE 185 AA; 20099 MW; A2P91716DF023179 CRC64;
SQ

[illegible]

RESULT 2			
ID	PRELIMINARY:	PRT:	163 AA.
082086			
AC 082086;			
DT 01-NOV-1998 (TREMBLrel . 08, Created)			
DT 01-NOV-1998 (TREMBLrel . 08, last sequence update)			
DT 01-JUN-2002 (TREMBLrel . 21, last annotation update)			
DE Pathogenesis related protein-1.			
GN pr-1.			
OS zea mays (maize).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;			
OC Panicoideae; Andropogonaceae; zea.			
OX NCBI_TaxID=4577;			
RN [1]			
RP SEQUENCE FROM N.A.			
R6 MEDLINE=98313983; PubMed=9650297;			
RA Morris S.W., Vernooij B., Tiltman S., Starrett M., Thomas S.,			
RA Wiltie C.C., Frederiksen R.A., Bhandufalck A., Hulbert S., Ukens S.;			
RT "Induced resistance responses in maize.";			
RL Mol. Plant Microbe Interact. 11:643-658(1998).			
DR EMBL: U87200; AAC25629.1; -.			
DR HSSP: P04284; 1CIE.			
DR InterPro: IPR001283; Allrgn_V5/Tpxl.			
DR Pfam: PF00188; SCP: 1.			
DR PRINTS: PR00837; V5TPXLKE.			
DR Prodom: PD000542; Allrgn_V5/Tpxl. 1.			
DR SMART: SM00198; SCP: 1.			
DR PROSITE: PS01009; SCP_A65_PRL_SCT_1; 1.			
DR PROSITE: PS01010; SCP_A65_PRL_SCT_2; UNKNOWN_1.			
Q0 SEQUENCE 163 AA: 17224 MW: 8331850Fl3365219 CRC64;			

Query Match	30.5%	Score 331	DB 10	Length 163
Best Local Similarity	39.0%	Pred. No. 1,2e-17		
Matches	73	Conservative	21	Mismatches 61; Indels 32; Gaps 6
OY	20	ACLLIATLTLACAPAPTHGARYLMEGGAAYTKAQQSGTSGSNATADEYLAPHNOARA	79	
			:	
6b	6	ACLLIATAIIVAPPC-----TAQNSFOD--YVPHNARA	39	
			:	

QY 80 AVGAAPLRMNNGLSAAAGTVAOORROGGCAFADVGASPYGANGMSASTYA--RPAEVA 137
 Db 40 DVGGPSPWSDTVAAYAQSYAAQ--RGDCCLKHSG-GPTGENIFWCSAADMASDPAVG 96
 QY 138 LMAVEGRYTHANNTCAGAGRCGTYTQVWMNTAEVSCAASCATGA-TLLCLYNPHGN 196
 Db 97 SWSSKQYIHDTNSCAGEGVCGHYTQVWMRDSATGICARVCDNNAGVFLICSYNPGN 156
 QY 197 VQGQSPY 203
 Db 157 VVGESPY 163

RESULT 3	09ZNX5	PRELIMINARY;	PRT; 191 AA.
ID	09ZNX5		
AC	09ZNX5;		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	PR-1-like protein precursor.		
GN	PR-1.		
OS	Camellia sinensis (Tea).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; Ericales; Theaceae; Camellia.		
OX	NCBI_TaxID=4442;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PISTIL;		
RA	Tomimoto Y., Yamaguchi S., Ogi Y., Nagatomi S., Ikehashi H.,		
RA	Komyama Y.;		
RT	"Polymorphism of PR-1-like proteins detected in pistil of Camellia.";		
RL	Breeding Sci. 46:293-293(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PISTIL;		
RA	Tomimoto Y., Ikehashi H., Kakeda K., Komyama Y.;		
RT	"A pistil-specific PR-1 like protein of Camellia, its expression,		
RT	sequence and genealogical position.";		
DR	EMBL: AB015047; BAA34937.1; -.		
DR	HSP; P04284; 1CFE.		
DR	InterPro: IPR001283; Allrgn_V5/TPx1.		
DR	Pfam: PF00188; SCP; 1.		
DR	ProDom: PD000542; Allrgn_V5/TPx1; 1.		
DR	SMART: SM00198; SCP; 1.		
KW	Signal.		
ET	1	36	POTENTIAL.
SEQ	SEQUENCE 191 AA; 21591 MW; 6764CCAB8CBF0467 CRC64;		

	Query Match:	30.0%;	Score 325.5;	DB 10;	Length 191;	
	Best Local Similarity:	38.7%;	Pred. No. 3,7e-17;			
	Matches	75;	Conservative	25;	Mismatches 61;	Indels 33; Gaps 8;
QY	22	LLATLTLALCAADAPTH-----GARVLMPGAGAVTKAQGGTSGSNAITADEYLAPH	74			
		: : :	: :			
Dd	19	ILPVLIVLIC--HSSHTLADHPRIARWVPG-----AARCEVDAAH	57			
QY	75	NQAANAAGVAFPLEWNNGCLASAAAGTVAAOORRGCGCAFADY--GASPYGANGCMASYBAR-P	132			
		: : : :	: : : :			
Dd	58	NSAAAEAGVDPLKMWSTSLNAAASRLVRFOKNMHCFFEDMTGLQLQYSNOMMSDYSKRP	117			
		: : : :	: : : :			
QY	133	AEEVALLVABEG--RYRYHANNTCAAGRCOGCTGYOVWRNTAEVGCAQASCA--TGATLTFLC	190			
		: : : : : :	: : : :			
Dd	118	REVEEYVWNSGRKKHYTYTNICYVRNONGCPKYQVVWMENTEWYGCAQGVCCNNNGSLISCF	177			
QY	191	YNPH-GAVGOSPPY	203			
		:	: : :			
Dd	178	YYPHGNIIGGPORY	191			

RESULT 4

```

O9XH05
ID Q9XH05 PRELIMINARY; PRT; 164 AA.
AC Q9XH05;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE T1N24.14 protein.
GN T1N24.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Washu;
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The sequence of A. thaliana T1N24."
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF149413; AAD40121.1; -.
DR HSSP: P04284; ICFF.
DR InterPro: IPR001283; Allrgn_V5/TpX1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TpX1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
SQ SEQUENCE 164 AA; 18397 MW; 840F99DB9FA7DF39 CRC64;

Query Match
Best Local Similarity 46.3%; Score 313.5; DB 10; Length 164;
Matches 63; Conservative 18; Mismatches 52; Indels 3; Gaps 3;

OY 69 EYLAPHNQARAAGVAPLWMNAGLASAAAGTAAQOROGCGAFADVGASP-YGANQGMAS 127
DB 31 DYLDENNRARTQGVPPMKWANG-AEQYAMNAAQQR-GDCSLTSHNSNGLYGENTLANS 88
OY 128 YARAPAEVALVVAEGRIYTHANNNTCAAGROCGTYTVVWRNTAEVGCQAQSCATGATLT 187
DB 89 GALSGEAEVKLVVWNEKSDIYASNTCSDGKOGCHYTQVWVRTSEWVGCAKVCNDGTFEV 148
OY 188 LCLYNPHGNVQOSPY 203
DB 149 TCNYTPPGNYRGKRMYP 164

RESULT 5
O8W084 PRELIMINARY; PRT; 167 AA.
AC O8W084;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative pathogenesis-related protein.
GN OSJNB0091E23.7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNB0091E23."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AP003853; BAB84473.1; -.
DR InterPro: IPR001283; Allrgn_V5/TpX1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TpX1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; UNKNOWN.1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; UNKNOWN.1.
SQ SEQUENCE 167 AA; 18334 MW; 40AE3EA728443D2E CRC64;

Query Match
Best Local Similarity 40.1%; Score 309; DB 10; Length 167;
Matches 73; Conservative 21; Mismatches 68; Indels 20; Gaps 7;

OY 25 ATLALCAAPPTHGARYLMPGAGAYTKAQQGTGSGSNATADEYLAIPHNAARAAGVA 84
DB 3 ASKLALICS-----LFLV-----AVVAATMFHCSDAQNSPQD-YLSPQNAARSAGVYG 48
OY 85 PLRWNAGLASAAGTAAQOROGCGAFADVGASPYGANGQASVRA--RAEYVALVVAE 142
DB 49 PMSNSTKLGFAEDYARQ--RKGDCLQHSG-GPYGENIFWGSAGADWTADAVRSWDE 105
OY 143 GRYTTHANNNTCAAGROCGTYTVVWRNTAEVGCQAQASC-ATGATLTCLYNPHGNVQOS 201
DB 106 KKYNYASNSCAAGKVCGHYTQVWVRDSTNVGCARVGCDNRGFIICNTEPKNITVGR 165
OY 202 PY 203
DB 166 PY 167

RESULT 6
O43489 PRELIMINARY; PRT; 164 AA.
AC O43489;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE PR-1a pathogenesis related protein (Hv-1a) precursor.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OX Trifliceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PALLAS; TISSUE=LEAF;
RX MEDLINE=94281675; PubMed=8012045;
RA Bryngelsson T., Sommer-Knudsen J., Gregersen P.L., Collinge D.B.,
RA Ek B., Thordal-Christensen H.;
RT "Purification, characterization and molecular cloning of basic PR-1-
RT type pathogenesis related proteins from barley."
RL Mol. Plant Microbe Interact. 7:267-275(1994).
DR EMBL: X74939; CA52893.1; -.
DR HSSP: P04284; ICFF.
DR InterPro: IPR001283; Allrgn_V5/TpX1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TpX1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Signal.
FT SIGNAL 1 24
CHAIN 25 164 PR-1A PATHOGENESIS RELATED PROTEIN
FT CHAIN 25 164 (HV-1A).
SQ SEQUENCE 164 AA; 17440 MW; 063F219DEF7E548 CRC64;

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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150864.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156548.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157653.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158323.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.

PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 32.1%; Score 348.5; DB 21; Length 185;
Best Local Similarity 48.3%; Pred. No. 1,5e-24;
Matches 69; Conservative 17; Mismatches 54; Indels 3; Gaps 2;

QY 64 NATDEYLAPHNORAAVGAFLRMNAGLASAAGTVAOORGGCGAFADVGASPYGANO 123
DB 43 SAAKAFPTDAHNNKARAWGVPLVWSOTLERAAASRLARTQRNOKCFEASLNPCKTGANO 102
QY 124 GWAS--YRARPAAEVVALVAEGRYTHANNTCAGRCGCTYTTQVWRNTAEVGAQASCA 181
DB 103 LMAKGLVAVPTSLAVETVWKEKEPEYNYKSDTCAANHTCGYKQVWRNSKEIGCAQATCT 162
QY 182 TGAAT-LTLCILYHPHGNVGOOSPY 203
DB 163 KESTVLTICFYNPNGNVIGQKPY 185

RESULT 3
ID AAG15732
AC AAG15732; standard; Protein; 185 AA.
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16100.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
OS
XX
PM EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123588.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.

PR 21-OCT-1999; 9905-0160815.
PR 22-OCT-1999; 9905-0160980.
PR 22-OCT-1999; 9905-0160981.
PR 22-OCT-1999; 9905-0160989.
PR 25-OCT-1999; 9905-0161404.
PR 25-OCT-1999; 9905-0161405.
PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.

Query Match 32.0%; Score 347.5; DB 21; Length 185;
Best Local Similarity 47.6%; Pred. No. 1.9e-24;
Matches 68; Conservative 18; Mismatches 54; Indels 3; Gaps 2;

OY 64 NATADEYLAPHNOCRAAAGVAPLPMNAGLASAAAGTVAGQRRGSCAFADYGASPYGANQ 123
DB 43 SAAKAFIDAHNKRRAWGVPLVMSQTLAAASRLARQNRQKKCEPASIIPGKYGANQ 102
OY 124 GWAS--TRAPAEVVALVMAEGRYTHANNTCAGRCGCTTYQVYWRNTAEVGAQASCA 181
DB 103 LMAAGLVAVTPSLAVETWKEKPEFYVKSDTCANHTCGVYKQVYWRNSKELGCAQATCT 162
OY 182 TGAAT-LTLCLYNPHGNVQOSPY 203
DB 163 KESTVLTICFPNPGNITGOKPY 185

RESULT 4

AAK91595
ID AAK91595 standard; Protein; 163 AA.

XX AAK91595;

DT 20-JUN-1996 (first entry)

DE PR-1 like protein PR-1mz.

XX SAR; tobacco; protein-synthesis independent gene; cyclohexamide;
KW systemic acquired resistance response; anti-pathogen; plant protection;
KM maize; PR-1.

XX Zea mays.

OS W09519443-A2.

PN 20-JUL-1995.

PF 03-JAN-1995; 95WO-IB00002.

PR 13-JAN-1994; 94US-0181271.

XX (CIBA) CIBA GEIGY AG.

PI Alexander DC, Ryals JA, Uknes SJ, Ward ER;

XX WPI; 1995-263872/34.

DR N-PSDB; AAO99804.

PT New DNA contg. plant systemic acquired resistance genes - and
transgenic plants contg. them, impart disease and pest resistance,
also Arabidopsis gene promoter to control DNA transcription

XX Claim 21; Page 70-71; 85pp; English.

CC This sequence represents the maize PR-1 like protein, PR-1mz. The cDNA
encoding this sequence was isolated by screening a BtH-induced cDNA
library of maize. The library was screened using a probe matching to
CC the PR-1 barley clone HVPRI8R. The cDNA encoding this sequence,

CC AAO99800-Q99803 and AAO99805 are all used in recombinant/chimeric DNA
CC molecules of the invention. The DNA sequences were isolated by
CC differential screening of a cDNA library, followed by analysis by
CC Northern hybridisation to RNA in the presence and absence of
CC cyclohexamide. The genes are used in the creation of transgenic plants.
CC All of these sequences confer anti-pathogenic properties to transgenic
CC plants. Transgenic expression of 2 or more of the recombinant molecules
CC of the invention that encode anti-pathogenic proteins provides a
CC synergistic increase in plant protection, and may also offer protection
CC against a wider range of pathogens.

XX Sequence 163 AA;

Query Match 30.5%; Score 331; DB 16; Length 163;
Best Local Similarity 39.0%; Pred. No. 5.6e-23;
Matches 73; Conservative 21; Mismatches 61; Indels 32; Gaps 6;

OY 20 ACLLATLTLALCAAPAPPTHGARYLMPGAGAVTKAQGGTSGSNATADEYLAPHNOCARA 79
DB 6 ACLLATLMAAIVVAPC-----TAQNSPOD-YVDEHNARA 39
OY 80 AVGVAPLRMNAAGLASAAAGTVAGQRRGSCAFADYGASPYGANGMASYRA--RPAEYVA 137
DB 40 DVGAGPVSMDTYVAATAGSTAAO--RQDCKLIHSG-GPTGENLFWSAGADWSASDAVG 96
OY 138 LMAEGRYTHANNTCAGRCGCTTYQVYWRNTAEVGAQASCATGA-TTLCLYNPHGN 196
DB 97 SWVESEKQYDHDRTNSCAEGVCGHYQVWRDSTAIGCARVVCNMGVFLICSYNPPGN 156
OY 197 VQGGOSPY 203
DB 157 VVGESPY 163

RESULT 5

AAV29944
ID AAV29944 standard; Protein; 163 AA.

XX AAV29944;

DT 22-NOV-1999 (first entry)

DE Zea mays pathogenesis-related class I PR-183 protein.

XX Zea mays; maize; pathogenesis-related class I; PR-1; promoter;
KW regulation; expression; disease resistance; genetic manipulation;
KW tobacco mosaic virus; cucumber mosaic virus; ringspot virus;
KW necrosis virus; maize dwarf virus; viroid; bacterial; insect;
KW nematode; fungal.

XX Zea mays.

OS W09943819-A1.

PN 02-SEP-1999.

PF 11-FEB-1999; 99WO-US03011.

PR 26-FEB-1998; 98US-0076100.

PR 27-MAR-1998; 98US-0079648.

XX (PION-) PIONEER HI-BRED INT INC.

PI Crane VC;

XX WPI; 1999-527621/44.

DR N-PSDB; AAZ21207.

PT New promoter sequences from pathogenesis-related genes of maize -
XX Example 3; Page 73-74; 86pp; English.

CC AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters

CC isolated from a family of maize (*Zea mays*) genes encoding pathogenesis
CC related (PR-1) proteins. The promoters are useful for expressing
CC heterologous genes (including genes for disease resistance) in plants,
CC especially dicots, or monocots i.e. maize. The promoters are useful for
CC the genetic manipulation of plants to exhibit specific phenotypes,
CC particularly enhanced resistance to pathogen-caused disease. Pathogens
CC include viruses such as tobacco or cucumber mosaic virus, ringspot
CC virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,
CC insects, nematodes and fungi. The present sequence represents a maize
CC PR-1 protein given in the present invention.

XX Sequence 163 AA;

Query Match 30.5%; Score 331; DB 20; Length 163;
Best Local Similarity 39.0%; Pred. No. 5,6e-23;

Matches 73; Conservative 21; Mismatches 61; Indels 32; Gaps 6;

QY 20 ACLLATLALCAAPAPFHGAVLMPGAGAVTKAQQGGTSSSMTADEYLAPHNORA 79
DB 6 ACLLALMAAIVVAPC-----TAAQNSPD-YVDPHMAARA 39
QY 80 AVGAAPLRNAGIASAAAGTVAQORROGCAFDVGCASPYGANGWASYRA--RPAEVVA 137
DB 40 DYGVGVSWDPTVAAYAQSYAAQ--RQDQQLHSG-GPYGENLFWGSAGADMSADAYG 96
QY 138 LWVAGRYTTHANNITCAAGRCGCTTYOVVRNTAEVGCQAQASCATGA-TLTICLYNPHGN 196
DB 97 SWVSEKQYDHPTNSCAGGVCGHYTQVWRDSTHTGACARVCDNNAVGFITCSYNPEN 156
QY 197 VQGSPY 203
DB 157 VVGESPY 163

RESULT 6
ABR77767
ID ABR77767 standard; Protein; 162 AA.

XX ABR77767;

DT 20-AUG-2002 (first entry)

XX Amino acid sequence of an antibacterial protein.

DE Antibacterial protein; microbe resistance; plant.

XX Elaeis guineensis.

PN JP2002095477-A.

PD 02-APR-2002.

XX 20-SEP-2000; 2000JP-0285905.

PF 20-SEP-2000; 2000JP-0285905.

PR 20-SEP-2000; 2000JP-0285905.

XX (MITU) MITSUBISHI CHEM CORP.

PA (BADA-) BADAN PENGKRAJIAN DAN PENKERAPAN TEKNOLOGI.

PA (BIOT-) BIOINDUSTRI KYOKAI SH.

PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.

XX WPI; 2002-439987/47.

DR N-PSDB; ABL59008.

XX New protein and its gene, useful for creating plants with high

PT resistance to pathogenic microbes -

XX Claim 1; Page 9-10; 13pp; Japanese.

XX The present sequence represents a polypeptide which has antibacterial

CC activity. The antibacterial protein and its polynucleotide can be used

CC for the creation of a plant with resistance against pathogenic microbes.

XX Sequence 162 AA;

Query Match 29.7%; Score 322; DB 23; Length 162;
Best Local Similarity 45.6%; Pred. No. 3,8e-22;
Matches 62; Conservative 22; Mismatches 48; Indels 4; Gaps 3;

QY 69 EYLAPHNORAAVGAAPLRNAGIASAAAGTVAQORROGCAFDVGCASPYGANGWASY 128
DB 30 DEVSANMAARAAGVGPVSMNTVAAYANVANO--RIGDQQLVHSG-GPYGENLFWGSG 86
QY 129 RA-RPAEVVALMWAGRYTTHANNITCAAGRCGCTTYOVVRNTAEVGCQAQASCATG 187
DB 87 REYTAADAVNLMVSEKQWYDYSTWTCAGAVCGHYTQVWRDSTHTGACARVKNCSGALPT 146
QY 188 ICLYNPHGVQSPY 203
DB 147 ICNKPQGNIVGQREY 162

RESULT 7
AAG47493
ID AAG47493 standard; Protein; 127 AA.

XX AAG47493;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 59867.

DE Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123160.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140981.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142972.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
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PR 28-OCT-1999; 99US-0161920.
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Query Match 29.0%; Score 314.5; DB 21; Length 127;
 Best Local Similarity 48.4%; Pred. No. 1.4e-21;
 Matches 61; Conservative 15; Mismatches 47; Indels 3; Gaps 2;

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QY 81 VGVADLRNNAGLASAAAGTYAQQROGCAFDADVGASPYGANQGNAS--YRRAPAEVAL 138
DB 2 VGVPELVMSQTLFAASRLARQYRMOKCEFASINRGKYGANQWAKGIVAVTSLAVET 61
QY 139 WVAEGRYTTHANNPCAGROCGTYTGVWVHNTAEVGCASQASCATGAT-LTLCIYNPHGNV 197
DB 63 WKKEKPFYNYKSDPCANHTCGYKQVYWRNSRELCAQATCTKRISTYLTICFNPONI 121
QY 198 QGQSPY 203
DB 122 IGQKPY 127

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RESULT 9

ABR77765 standard; Protein; 161 AA.

ABR77765;

20-AUG-2002 (first entry)

Amino acid sequence of an antibacterial protein.

Antibacterial protein; antibacterial agent; food; plant.

Wasabia japonica.

JP2002095475-A.

02-APR-2002.

19-SEP-2000; 2000JP-0284178.

19-SEP-2000; 2000JP-0284178.

(IWAT-) IWATE KEN.

WPI; 2002-439986/47.

N-PSDB; ABL59001.

New antibacterial protein gene of Wasabia japonica -

Claim 1; Page 13-14; 17pp; Japanese.

The present sequence represents an antibacterial protein of Wasabia

japonica. The protein can be used in an antibacterial agent and a

functional food.

Sequence 161 AA;

Query Match 28.0%; Score 304; DB 23; Length 161;

Best Local Similarity 39.8%; Pred. No. 1.8e-20;

Matches 72; Conservative 20; Mismatches 61; Indels 28; Gaps 7;

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QY 23 LIALTLALCAAPAPTHGARVLMPGAGAVTKAQQGTGSGSNATADEVYLAPHNORAAV 82
DB 9 LILIALALVGA-----IVLP-----SKAD-----SQDYLRVHNGRAAVG 45
QY 83 VAPLRNNAAGLASAAAGTYAQQROGCAFDADVGASPYGANQGNASTRARPAEVALVAE 142
DB 46 VSPMOWDDRYA-AFARSYADRR-GDCRLTHSG-GPYGRLMGSSDLSGISAVMMWNE 102
QY 143 GRYTTHANNPCAGROCGTYTGVWVHNTAEVGCASQASCATGATLTLCIYNPHGNVQOSP 202

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Db 103 KANYTPSNTC--NGVCCHTQVWRNSVRLGCAKVRKNNGGTIIYCNIDPFGNYNQRP 160
 QY 203 Y 203
 Db 161 Y 161

RESULT 10

AAFP1059
 ID AAFP1059 standard; protein; 168 AA.

XX
 AC AAFP1059;

DT 21-JUN-1990 (first entry)

XX Nicotiana tabacum pathogenesis-related (P-R) protein encoded by cDNA.

DE Nicotiana tabacum pathogenesis-related protein; Nicotiana tabacum cv. Samsun NN;

KW PNTSNNCPRLC/83.

OS Nicotiana tabacum cv. Samsun NN.

XX
 FH Key Location/Qualifiers

FT Peptide 1..30 /note="Signal peptide"

FT Protein 31..168

XX
 PN EP307841-A.

PD 22-MAR-1989.

PF 12-SEP-1988; 88EP-0114877.

PR 15-SEP-1987; 87US-0096579.

XX
 PA (GEHO-) GEN HOSPITAL CORP.

XX
 PI Pflitzner UM, Pflitzner AP, Goodman HM;

XX
 DR WPI; 1989-087235/12.

PT Pathogenesis-related proteins and regulatory sequences -
 used for expression in plants to enhance hypersensitive response
 to invading pathogen

XX
 PS Fig 4; : 32pp; English.

CC It is deduced from cDNA from tobacco mosaic virus (TMV) infected
 CC tobacco plants contained in plasmid pNCSNNCPRLC/83. Expression of
 CC a recombinant DNA molecule that encodes P-R proteins and
 CC regulatory sequences in a plant enhances the hypersensitive response of
 CC the plant to an invading pathogen. The calculated molecular weight of
 CC the mature P-R protein is 15,129 and is in reasonable agreement with the
 CC M of 18kD estimated by SDS polyacrylamide gel electrophoresis.

XX
 SQ Sequence 168 AA:

Query Match 28.0%; Score 304; DB 10; Length 168;

Best Local Similarity 45.0%; Pred. No. 1.9e-20; Mismatches 50; Indels 12; Gaps 3;

QY 69 EYLAPHNOARAAYGAPLWMNGLASAAAGTYAQQRRGGCAFADVGA---SPYGANOG 124

Db 36 DYLDANTARADYGEPLTWDMGVAAYQNTYASQ-----LAADCNLVHSHQYGENLA 88

QY 125 WASYR-ARPAEVVALWVAEGRYTHANNTCAGRCGTYTQVWRNTAEVGAQAQASCATG 183

Db 89 WGSGBDELTAAKAVEMWVNEKQYTHADSNITCAQGVCGHYTQVWRNSVRYGCAKRYCCNN 148

QY 184 AFLTLCLYNPHGNVQGSQSPY 203

Db 149 GYVSCNIDPFGNYTGSQSPY 168

RESULT 11

AAAR07314

ID AAR07314 standard; protein; 138 AA.

XX
 AC AAR07314;

DT 31-JAN-1991 (first entry)

XX PR-1b plant pathogenesis-related protein.

XX Transgenic plants; disease resistance; chimeric DNA;

KW plant pathogenesis-related protein.

XX
 OS synthetic.

PN EP392225-A.

PD 17-OCT-1990.

PF 21-MAR-1990; 90EP-0105336.

PR 20-OCT-1989; 89US-0425504.

PR 24-MAR-1989; 89US-0329018.

XX
 PA (CIBA) CIBA GEIGY AG.

XX
 PI Ryals JA, Alexander DC, Goodman RM, Melius F, Payne GB;

XX
 PI Stinson JR, Neuhaus J-M, Moyer MB;

XX
 DR WPI; 1990-313983/42.

XX
 DR N-PSDB; AAQ06181.

PT Disease-resistant transgenic plants - obt'd. using encoding an

XX inducible pathogenesis-related protein from infected plants.

XX
 PS Example 15; page 22; 77pp; English.

CC This is the sequence of the plant pathogenesis-related protein
 CC (PRP), PR-1b. It confers systemic acquired resistance to plants.
 CC The corresp. DNA is used, in a chimeric construct, to produce
 CC transgenic plant cells or -tissues with the ability to regenerate
 CC into plants which are disease resistant.

XX See also AAQ06179-80, AAQ06182-86, AAQ06199-Q06208 and AAQ06829.

XX
 SQ Sequence 138 AA:

Query Match 27.9%; Score 303; DB 11; Length 138;

Best Local Similarity 46.1%; Pred. No. 1.8e-20; Mismatches 47; Indels 14; Gaps 4;

QY 69 EYLAPHNOARAAYGAPLWMNGLASAAAGTYAQQRRGGCAFADVGA---SPYGAN-- 122

Db 6 DYLDANTARADYGEPLTWDMGVAAYQNTYASQ-----LAADCNLVHSHQYGENLA 58

QY 123 OGMAVYRARPAAEVVALWVAEGRYTHANNTCAGRCGTYTQVWRNTAEVGAQAQASCAT 182

Db 59 QGSDDEFT-AAKAVEMWVNEKQYTHADSNITCAQGVCGHYTQVWRNSVRYGCAKRYCCNN 117

QY 183 GATLTLCLYNPHGNVQGSQSPY 203

Db 118 GGYVSCNIDPFGNYTGSQSPY 138

RESULT 12

AAAY44003

ID AAY44003 standard; protein; 139 AA.

XX
 AC AAY44003;

DT 21-DEC-1999 (first entry)

PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0122348.
PR 22-MAR-1999; 99US-0125788.
PR 23-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
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PR	26-OCT-1999;	99US-0161359.
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PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

[illegible]

XX	RESULT 15
XX	AA0808224
ID	AA0808224 standard; protein: 138 AA.
XX	
AC	AA0808224;
DT	31-JAN-1991 (first entry)
XX	
DE	PR-1c plant pathogenesis-related protein.
XX	
KW	Transgenic plants; disease resistance; chimeric DNA
KW	plant pathogenesis-related protein.
XX	
OS	synthetic.
XX	
PN	EP392225-A.
XX	
PD	17-OCT-1990.
XX	
PF	21-MAR-1990; 90EP-0105336.
XX	

PR 20-OCT-1989; 89US-0425504.
 PR 24-MAR-1989; 89US-0329018.
 PR 20-JUN-1989; 89US-0368672.
 FA (CIBA) CIBA GEIGY AG.
 XX
 XX
 PI Ryals JA, Alexander DC, Goodman RM, Melius F, Payne GB;
 PI stinson JR, Neuhaus J-M, Moyer MB;
 XX
 XX WPI; 1990-313983/42.
 DR N-PSDB; AAQ06182.
 XX
 XX Disease-resistant transgenic plants - obtd. using encoding an
 PT inducible pathogenesis-related protein from infected plants.
 PT
 XX
 XX Example 15; page 22; 77pp; English.
 XX
 XX This is the plant pathogenesis-related protein (PRP), PR-1c. It
 CC confers systemic acquired resistance to plants. The corresp. DNA
 CC is used, in a chimeric construct, to produce transgenic plant cells
 CC or -tissues with the ability to regenerate into plants which are
 CC disease resistant.
 CC See also AAQ06179-81, AAQ06183-86 and AAQ06199-Q06208.
 CC
 XX Sequence 138 AA;
 XX

	Query Match:	27.3%	Score	296;	DB	11;	Length	138;
	Best Local Similarity	44.3%;	Pred.	No.	8.1e-20;			
	Matches	62;	Conservative	15;	Mismatches	51;	Indels	12;
					Gaps			3;
QY	69	EYLAPHNQAAAGVAPLRFMNGLSAAAGTADQRROGGCAFADYGA----	SPYGANOG	124				
	:	: :	:	:	:	:	:	:
Db	6	DYLDHNHTARADVGEPFLTWDDQVAAYAQNVASQ-----	LAMDCLVLVSHHQYEINLA	58				
QY	125	WASTR-ARRPAEVVALMVAEGRTYYTHANNITCAARGOCCTGYTVWRNTAEVCAQAOSCATFG		183				
	:	: : : : : : : : : : : : : : : : :						
Db	59	WGSGDEFLTAKAEMVNVEKEQYIARDHSNTCAQGCGCHTYGVWRNSRVGVCARVQCNNNG		118				
QY	184	ATLLTLCLYNPHGNVOGSPPY	203					
	:	: : : : : : : : : : : : : : : :						
Db	119	GIYVSCNYPDPCGNVIKSPSY	138					

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Search completed: March 19, 2003, 09:36:50
Job time : 38 secs
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CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 139
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: tobacco
FEATURE: pathogenesis related protein; Table 16 Row 6
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Cutt, J. R.
AUTHORS: Dixon, D. C.
AUTHORS: Carr, J. P.
AUTHORS: Klessig, D. F.
TITLE: Isolation and nucleotide sequence of cDNA clones for the
TITLE: pathogenesis related proteins of Nicotiana glauca induced by TMV
TITLE: infection.
JOURNAL: Nucleic Acids Research
VOLUME: 16
PAGES: 9861
DATE: 1988
IS-07-857-224B-102

```

Query Match:          27.9%   Score 303; DB 2; Length 139;
Best Local Similarity 46.1%; Pred. No. 3.4e-24;
Matches    65; Conservative    15; Mismatches    47; Indels    14; Gaps    4.

QY      69 EYLAPHNQARAAGVAPLRLRMNAGLSAQAAGTVAOQRROGGCAFADGCA---SPYGAN--122
       1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
Db      7 DYLDHNHTARADGVGEPLTWMDNGVAAIYKQNTYSQ-----LADCNLIYHSHQYGENLA 59
       1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

QY      123 QGMASRYRARPAEVVALVMAEGRIYYHANNTCAAGHCGCTTYQVVWVRMTAEVGCAQAQASCAT 182
       1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
Db     60 QGSDEFWT-AAKAVEMVMVEDEKQYDHDSDNTCAQGQVCGHYTQVWRMSRVGCARAYCKNN 118
       1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

QY      183 GATITLTCLTYPHSGNVGOQSPT 203
       1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
Db     119 GCYVSCNDPDPGNVIGOSPT 139
       1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

RESULT 3
US-07-857-224B-104
; Sequence 104, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none

```

1 COUNTRY: Switzerland
2 ZIP: (note: this is an international post code) CH-8092
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
6 COMPUTER: Apple Macintosh
7 OPERATING SYSTEM: Macintosh 7.0
8 SOFTWARE: Microsoft Word
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/07/857,224B
12 FILING DATE: 03/25/92
13 CLASSIFICATION: 436
14
15 PRIOR APPLICATION DATA: none
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (international) 41 1 632 2830
18 TELEFAX: (international) 41 1 262 2437
19
20 TELEX: none
21
22 INFORMATION FOR SEQ ID NO: 104:
23
24 SEQUENCE CHARACTERISTICS:
25
26 LENGTH: 141
27 TYPE: amino acid
28 TOPOLOGY: linear
29
30 MOLECULE TYPE: protein
31
32 DESCRIPTION: protein
33
34 ORIGINAL SOURCE:
35 ORGANISM: maize
36
37 FEATURE: pathogenesis related protein; Table 16 Row 8
38 PUBLICATION INFORMATION:
39
40 AUTHORS:
41
42 AUTHORS: Cutt, J. R.
43
44 AUTHORS: Dixon, D. C.
45
46 AUTHORS: Carr, J. P.
47
48 AUTHORS: Klessig, D. F.
49
50 TITLE: Isolation and nucleotide sequence of cDNA clones for the
51 TITLE: pathogenesis related proteins of Nicotiana glauca induced by TMV
52 TITLE: infection.
53
54 JOURNAL: Nucleic Acids Research
55
56 VOLUME: 16
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58 PAGES: 9861
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60 DATE: 1988
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27.6%; Score 299; DB 2; Length 141;
Best Local Similarity 42.4%; Pred. No. 9,2e-24;
Matches 61; Conservative 16; Mismatches 61; Indels 6; Gaps 4;

QY 63 SNADEIYLAPHNQAAANGVAPLEPRMNAAGLSAANAAGTYADQRRGGCAFEDVASPIYGAN 122
 : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SESSPDLYLPONSASARAANGVPWTWSTKLOFEEKYAAQ--RAGDCRLHSG-GPYGEN 57

QY 123 QGW--ASYRAARPAYVALVAAGRYTFTANNNTCAAGROCGTYGTGVNVRNTAEVGCQAASC 180
 : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 IFMSAGFEIMKAVDAYSRVWDEKMÖYNATNTSCAAGKVCGHYTQVVMRAVTTSIGCARVYC 117

QY 181 ATG-ATTITCLTNPHGNVOGOSPY 203
 : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 RDNKGVFILCNPEPKNIGMKPY 141

RESULT 4
US-07-857-224B-100
Sequence 100, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092


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1      INFORMATION FOR SEQ ID NO: 45:
2      SEQUENCE CHARACTERISTICS:
3          LENGTH: 168 amino acids
4          TYPE: amino acid
5          TOPOLOGY: linear
6      MOLECULE TYPE: protein
7      US-08-181-271A-45
8
9      Query Match          26.4%; Score 286; DB 1; Length 168:
10     Best Local Similarity 36.7%; Pred. No.2.6e-22;
11     Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps
12
13     QY 22 LLATLTLALCAADAPPHGAVRLMPGAGAVTKAQQGGTGGSSMATADEYLAPHNQAARAV 81
14         ||::||| :| | :||
15     Db 13 LTVSTLLFLFLVI---SHSCR-----AQNQQ-----DYLDHHTATRADV 48
16
17     QY 82 GVAFLRNAGLAAAGATVAAQQRGGCAFDVGA---SPYGAN--QGMASTRARARV 135
18         || | | | :| :| | | | | | | | | | | | | | | | | | | | | | | | | |
19     Db 49 GVEPLTWDDVDAVIAQNTYASQ-----LAADCNLVHSHGOTGENLADGSDFFWT-AAKA 100
20
21     QY 136 VALVVAEGRRYTHANNTCAGRCGTYGYVWRNTAEVCAQASCATGATLTLCLYNPHG 195
22         :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
23     Db 101 VEMVWDQEKYYDHDSTCKAQGGVCGHYTYQVWRNRSRVGCAKRVQCNNGYVSCNYPDG 160
24
25     QY 196 NNGOSPEY 203
26         | :| :| | |
27     Db 161 NYGSEPY 168
28
29 RESULT 6
30 US-08-449-315-45
31 : Sequence 45, Application US/08449315
32 : Patent No. 5650505
33 : GENERAL INFORMATION:
34 : APPLICANT: Ryals, John A.
35 : APPLICANT: Alexander, Danny C.
36 : APPLICANT: Beck, James J.
37 : APPLICANT: Duesing, John H.
38 : APPLICANT: Friedrich, Leslie B.
39 : APPLICANT: Goodman, Robert M.
40 : APPLICANT: Harms, Christian
41 : APPLICANT: Weins, JF., Frederick
42 : APPLICANT: Montoya, Alice
43 : APPLICANT: Moyer, Mary B.
44 : APPLICANT: Neuhaus, Jean-Marc
45 : APPLICANT: Payne, George B.
46 : APPLICANT: Sperison, Christoph
47 : APPLICANT: Stinson, Jeffrey R.
48 : APPLICANT: Uknes, Scott J.
49 : APPLICANT: Ward, Eric R.
50 : TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
51 : TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
52 : NUMBER OF SEQUENCES: 106
53 : CORRESPONDENCE ADDRESS:
54 : ADDRESSEE: CIBA-GEIGY Corporation
55 : STREET: 7 Skyline Drive
56 : CITY: Hawthorne
57 : STATE: New York
58 : COUNTRY: USA
59 : ZIP: 10532
60 : COMPUTER READABLE FORM:
61 : MEDIUM TYPE: Floppy disk
62 : COMPUTER: IBM PC compatible
63 : OPERATING SYSTEM: PC-DOS/MS-DOS
64 : SOFTWARE: Patent In Release #1.0, Version #1.25
65 : CURRENT APPLICATION DATA:
66 : APPLICATION NUMBER: US/08/449,315
67 : FILING DATE: 24-MAY-1995
68 : CLASSIFICATION: 800
69 : PRIOR APPLICATION DATA:
70 : APPLICATION NUMBER: 08/181,271
71 : FILING DATE: 13-JAN-94
72

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1  APPLICATION NUMBER: US 08/093,301
2  FILING DATE: 16-JUL-1993
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER: US 07/937,197
5  FILING DATE: 6-NOV-1992
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: US 07/678,378
8  FILING DATE: 1-APR-1991
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/305,566
11 FILING DATE: 6-FEB-1989
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/165,667
14 FILING DATE: 8-MAR-1988
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/042,847
17 FILING DATE: 6-APR-1993
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/632,441
20 FILING DATE: 21-DEC-1990
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/425,504
23 FILING DATE: 20-OCT-1989
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/848,506
26 FILING DATE: 6-MAR-1992
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/768,122
29 FILING DATE: 27-SEP-1991
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/580,431
32 FILING DATE: 7-SEP-1990
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 07/368,672
35 FILING DATE: 20-JUN-1989
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/329,018
38 FILING DATE: 24-MAR-1989
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 08/045,957
41 FILING DATE: 12-APR-1993
42 ATTORNEY/AGENT INFORMATION:
43 NAME: Elmer, James Scott
44 REGISTRATION NUMBER: 36,129
45 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
46 TELECOMMUNICATION INFORMATION:
47 TELEPHONE: (919)541-8614
48 TELEFAX: (919)541-8689
49 INFORMATION FOR SEQ ID NO: 45:
50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 168 amino acids
52 TYPE: amino acid
53 TOPOLOGY: linear
54 MOLECULE TYPE: protein
55 US-08-449-315-45
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APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,043
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT 1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19925/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-449-043-45
 Query Match 26.4%; Score 286; DB 1; Length 168;
 Best local similarity 36.7%; Pred. No. 2.6e-22;
 Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;
 QY 22 LILATLALCAPAPRPHGARVMEGAGAVYKKAQGGTSGSNATDEYLAIPNRAAY 81
 DB 13 LIVSTLLFLVLT--SHSCR-----AONSO-----DYDAHNTARADV 48
 QY 82 GVALRNMNGLASAAAGTVAQQRGGCAFADVGA---SPYGAN--QGWASYRARPAY 135
 DB 49 GVEPLTWMDQVAAYVQNVASQ-----LAADCNLVSHSGGYGENLAEGSGDFMT-AAKA 100
 QY 136 VALTVAEGRYTYHANTTCAGRCGCTTYQVYWRATVAGCAQASCATGATLTLCYNPHG 195
 DB 101 VEMVVDKQYDHDSTNCTAGQGVCGHYTVVWRNSVRVGCARVQCNGGTWVCNTDPG 160
 QY 196 NWQGSQPY 203
 DB 161 NYRGESPY 168
 RESULT 9
 US-08-456-265A-45
 Sequence 45, Application US/08456265A
 Patent No. 5767369
 GENERAL INFORMATION:
 APPLICANT: Alexander, Danny C.
 APPLICANT: Ryals, John A.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Stinson, Jeffrey R.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/456,265A
 FILING DATE: 31-MAY-95
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/181,271
 FILING DATE: 13-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988


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QY      22 LLATLLALCAAPPTIGARVLPNGAGAVTKQQGGSGSNATADELAIPHQAARAV 81
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1 RESULT 12
2 US-08-454-876-45
3 : Sequence 45, Application US/08454876
4 : Patent No. 5804693
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Ryals, John A.
9 : APPLICANT: Alexander, Danny C.
10 : APPLICANT: Beck, James J.
11 : APPLICANT: Duesing, John H.
12 : APPLICANT: Friedrich, Leslie B.
13 : APPLICANT: Goodman, Robert M.
14 : APPLICANT: Harms, Christian
15 : APPLICANT: Meins, Jr., Frederick
16 : APPLICANT: Montoya, Alice
17 : APPLICANT: Moyer, Mary B.
18 : APPLICANT: Neuhaus, Jean-Marc
19 : APPLICANT: Payne, George B.
20 : APPLICANT: Sperison, Christoph
21 : APPLICANT: Stinson, Jeffrey R.
22 : APPLICANT: Uknes, Scott J.
23 : APPLICANT: Ward, Eric R.
24 : APPLICANT: Williams, Shericca C.
25 :
26 : TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
27 : TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
28 : NUMBER OF SEQUENCES: 106
29 :
30 : CORRESPONDENCE ADDRESS:
31 : ADDRESSEE: CTBA-GEIGY Corporation
32 : STREET: 7 Skyline Drive
33 : CITY: Hawthorne
34 : STATE: New York
35 : COUNTRY: USA
36 : ZIP: 10532
37 :
38 : COMPUTER READABLE FORM:
39 : MEDIUM TYPE: Floppy disk
40 : COMPUTER: IBM PC compatible
41 : OPERATING SYSTEM: PC-DOS/MS-DOS
42 : SOFTWARE: Patentln Release #1.0, Version #1.25
43 :
44 : CURRENT APPLICATION DATA:
45 : APPLICATION NUMBER: US/08/454,876
46 : FILING DATE: 31-MAY-1995
47 : CLASSIFICATION: 435
48 :
49 : PRIOR APPLICATION DATA:
50 : APPLICATION NUMBER: 08/181,271
51 : FILING DATE: 13-JAN-94
52 : APPLICATION NUMBER: US 08/093,301
53 : FILING DATE: 16-JUL-1993
54 :
55 : PRIOR APPLICATION DATA:
56 : APPLICATION NUMBER: US 07/937,197
57 : FILING DATE: 6-NOV-1992
58 :
59 : PRIOR APPLICATION DATA:
60 : APPLICATION NUMBER: US 07/678,378
61 : FILING DATE: 1-APR-1991
62 :
63 : PRIOR APPLICATION DATA:
64 : APPLICATION NUMBER: US 07/305,566
65 : FILING DATE: 6-FEB-1989
66 :
67 : PRIOR APPLICATION NUMBER: US 07/165,667
68 : FILING DATE: 8-MAR-1988
69 :
70 : PRIOR APPLICATION DATA:
71 : APPLICATION NUMBER: US 08/042,847
72 :

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1      FILINDATE: 6-APR-1993
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: US 07/632,441
4      FILING DATE: 21-DEC-1990
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US 07/425,504
7      FILING DATE: 20-OCT 1989
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: US 07/848,506
10     FILING DATE: 6-MAR-1992
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: US 07/768,122
13     FILING DATE: 27-SEP-1991
14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER: US 07/580,431
16     FILING DATE: 7-SEP-1990
17     PRIOR APPLICATION DATA:
18     APPLICATION NUMBER: US 07/368,672
19     FILING DATE: 20-JUN-1989
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER: US 07/329,018
22     FILING DATE: 24-MAR-1989
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER: US 08/045,957
25     FILING DATE: 12-APR-1993
26     ATTORNEY/AGENT INFORMATION:
27     NAME: Elmer, James Scott
28     REGISTRATION NUMBER: 36,129
29     REFERENCE/DOCKET NUMBER: S-19825/PL/C/GC 1727
30     TELECOMMUNICATION INFORMATION:
31     TELEPHONE: (919)541-8614
32     TELEFAX: (919)541-8689
33     INFORMATION FOR SEQ ID NO: 45:
34     SEQUENCE CHARACTERISTICS:
35     LENGTH: 168 amino acids
36     TYPE: amino acid
37     TOPOLOGY: linear
38     MOLECULE TYPE: protein
39     US-08-454-876-45

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Query March      26.4%; Score 286; DB 1; Length 168;
Best Local Similarity 36.7%; Pred. No. 2,6e-22;
Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7

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OY    82 GVADPLRNNGIASAAGTVAAGORGGCAFDVGA----SPYGAN--QGMASTRARPAEV 135
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OY    136 VALVWAGRRYYTAANNNTCAAGROCCGYTOVVNRNTEAVGCAQASCATGATLTLCIYPHG 195
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OY    196 NVQOGSEY 203
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Db    161 NYKGESPY 168

RESULT 13
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; Sequence 45, Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedlich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
;
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APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericea C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,364
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
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 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
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 PRIOR APPLICATION DATA:
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 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
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 FILING DATE: 6-APR-1993
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 FILING DATE: 21-DEC-1990
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 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
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 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-457-364-45
 Query Match 26.4%; Score 286; DB 2; Length 168;
 Best Local Similarity 36.7%; Pred. No. 2,6e-22;
 Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;
 QY 22 LILATLALCAAPAPTHGARVIMPGAGAVTKAQQGCTGSGSNATADYLAAPHNORAAV 81
 DB 13 LILVSTLLFLVLI---SHSCR-----AQNSQQ-----DYLAHNTARADV 48
 QY 82 GVAELRWNAAGLASAAGTVAQQRQGGCAFDYGA---SPYGAN--QGMASYRRAPAEV 135
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 ; Sequence 45, Application US/08456262
 ; Patent No. 5851766
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesling, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericea C.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 09:37:17 ; Search time 16 Seconds

(without alignments)
678.302 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

Sequence: 1 MAHSRSHHLLLPAPMATA.....ATLTLCLYNPHGNVQGSPPY 203

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Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1085	100.0	203	10 US-09-832-320-2	Sequence 2, Appl1
2	331	30.5	163	10 US-09-840-479-13	Sequence 13, Appl1
3	331	30.5	163	12 US-10-078-929-202	Sequence 202, App
4	300.5	27.7	171	9 US-10-068-347-4	Sequence 4, Appl1
5	287	26.5	164	12 US-10-078-929-82	Sequence 82, Appl1
6	287	26.5	176	12 US-10-078-929-86	Sequence 86, Appl1
7	280.5	25.9	167	12 US-10-078-929-100	Sequence 100, App
8	267	24.6	136	9 US-10-091-135-83	Sequence 83, Appl1
9	259.5	23.9	164	12 US-10-078-929-84	Sequence 84, Appl1
10	255	23.5	161	12 US-10-078-929-96	Sequence 96, Appl1
11	254	23.4	190	12 US-10-078-929-90	Sequence 90, Appl1
12	248	22.9	139	12 US-10-078-929-94	Sequence 94, Appl1
13	240	22.1	156	10 US-09-840-479-7	Sequence 7, Appl1
14	231	21.3	156	12 US-10-078-929-98	Sequence 98, Appl1
15	223.5	20.6	94	9 US-10-068-347-10	Sequence 2, Appl1
16	223.5	20.6	94	9 US-10-068-347-10	Sequence 10, Appl1
17	217.5	20.0	214	10 US-09-840-479-15	Sequence 15, Appl1
18	199	18.3	112	12 US-10-078-929-88	Sequence 88, Appl1
19	197	18.2	140	12 US-10-078-929-92	Sequence 92, Appl1

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21	193.5	17.8	455	9 US-09-944-403-50	Sequence 50, Appl1
22	193.5	17.8	455	9 US-09-944-896-50	Sequence 50, Appl1
23	193.5	17.8	455	9 US-09-944-944-50	Sequence 50, Appl1
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25	193.5	17.8	455	9 US-09-944-929-50	Sequence 50, Appl1
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27	193.5	17.8	455	10 US-09-944-449-50	Sequence 50, Appl1
28	193.5	17.8	455	10 US-09-944-457-50	Sequence 50, Appl1
29	193.5	17.8	455	10 US-09-944-862-50	Sequence 50, Appl1
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34	193.5	17.8	455	10 US-09-944-432-50	Sequence 50, Appl1
35	193.5	17.8	455	10 US-09-943-762-50	Sequence 50, Appl1
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37	193.5	17.8	455	10 US-09-944-851A-50	Sequence 50, Appl1
38	189.5	17.5	109	12 US-10-078-929-208	Sequence 208, App
39	188.5	17.4	446	9 US-10-042-141-47	Sequence 47, Appl1
40	188.5	17.4	446	10 US-09-726-643-47	Sequence 47, Appl1
41	188.5	17.4	446	10 US-09-790-264-2	Sequence 2, Appl1
42	179	16.5	420	10 US-09-790-264-4	Sequence 4, Appl1
43	177	16.3	463	9 US-09-905-291A-285	Sequence 285, App
44	177	16.3	463	9 US-09-902-853-285	Sequence 285, App
45	177	16.3	463	9 US-09-907-824-285	Sequence 285, App

ALIGNMENTS

RESULT 1
US-09-832-320-2
; Sequence 2, Application US/09832320
; Patent No. US20010049834A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Edmund H.
; TITLE OF INVENTION: Maize Pathogenesis-Related
; TITLE OF INVENTION: Polynucleotide and Methods of Use
; FILE REFERENCE: 35718/214291
; CURRENT APPLICATION NUMBER: US/09/832,320
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/195,801
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Zea mays
US-09-832-320-2

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Best Local Similarity	100.0%	Pred. No. 5.5e-85		
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DB	121	ANOGWASYPARPAEYVALWVAEGRYTTHANNCTACAGRCGTYYVWRTAEVGAQASC	180	
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; Sequence 13, Application US/09840479
; Patent No. US2001002580A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/840,479
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/257,583
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-09-840-479-13

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Query Match          30.5%; Score 331; DB 10; Length 163;
Best Local Similarity 39.0%; Pred. No. 3.7e-21;
Matches 73; Conservative 21; Mismatches 61; Indels 32; Gaps 6;

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    |||| : : : ||
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QY 197 VQGOSPY 203
    |||| : : : ||
DB 157 VVGESPY 163

```

```

RESULT 3
US-10-078-929-202
; Sequence 202, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Maao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BR1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11

```

```

; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 202
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-10-078-929-202

```

```

Query Match          30.5%; Score 331; DB 12; Length 163;
Best Local Similarity 39.0%; Pred. No. 3.7e-21;
Matches 73; Conservative 21; Mismatches 61; Indels 32; Gaps 6;

```

```

QY 20 ACLLATLALCAAPAPTHGARVLMPGAGAVTKAOGGTSGSNATADEYLAPHNOARA 79
    |||| : : : ||
    6 ACLALAMAATVAPC-----TAQNSPQD-YDPHNARA 39
    |||| : : : ||
QY 80 AVGAAPLRMNAGLASAAGTYAQQRRGGCAFADVGASPYGANQWASYRA--RPAEYVA 137
    |||| : : : ||
    40 DVGVPVSMDDTVAAAYQSYAAQ--RQGDCLIHSG-GPYGENLFMSGAGADMSASDAVG 96
    |||| : : : ||
QY 138 LMAVEGRYTHANTCAAGRCGCTTYQVWVRNTAEVGCQAQASCATGA-TLTLCYNPHGN 196
    |||| : : : ||
    97 SWSEKQYTHDHTNSCAEGQVCGHYTVWVRDSTAIGCARVYCDNNAGVFTICSYNPPGN 156
    |||| : : : ||
QY 197 VQGOSPY 203
    |||| : : : ||
DB 157 VVGESPY 163

```

```

RESULT 4
US-10-068-347-4
; Sequence 4, Application US/10068347
; Patent No. US2002016146A1
; GENERAL INFORMATION:
; APPLICANT: Pioneer HI-Bred International, Inc.
; APPLICANT: Simmons, Carl
; APPLICANT: Acevedo, Pedro
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Maize P1 Polynucleotides and Methods of Use
; FILE REFERENCE: 35718/242798 (5718-151)
; CURRENT APPLICATION NUMBER: US/10/068,347
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/267,052
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Zea mays
US-10-068-347-4

```

```

Query Match          27.7%; Score 300.5; DB 9; Length 171;
Best Local Similarity 41.9%; Pred. No. 1.5e-18;
Matches 70; Conservative 17; Mismatches 63; Indels 17; Gaps 7;
QY 42 VLMGAGAVTKAOGGTSGSNATADEYLAPHNOARAAGVAPLRNAGLASAAGTYA 101
    |||| : : : ||
DB 17 VVAAAAGRVYSAQN-----TAQDFVULHNSPRADYGVGNVAMNTIVA-AYAQSYA 66
    |||| : : : ||
QY 102 QORRGGCAFADVGASPYGANQW--ASRARPAEYVALMVAEGRYTHANTCAA--GR 157
    |||| : : : ||
DB 67 NQ-RAGDCRLVHSG-GPYGENLFMSGAGYAMTASNAVGSMAAEKROYNHAHTNCSAPSG 124
    |||| : : : ||
QY 158 QCGTITQVWVRNTAEVGCQAQASCATGA-TLTLCYNPHGNVQOSPY 203
    |||| : : : ||
DB 125 SCGHYTLVWRASSTAIGCARVYCSNNAAGVFTICNYPPGNVIGOSPY 171
    |||| : : : ||

```

RESULT 5

US-10-078-929-82

Sequence 82, Application US/10078929

Patent No. US20020152497A1

GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni

APPLICANT: Miao, Guo-Hua

APPLICANT: Falco, Saverio Carl

APPLICANT: Sakai, Hajime

APPLICANT: Famodu, Omolayo O.

APPLICANT: Odell, Joan T.

APPLICANT: Meyers, Blake

APPLICANT: Thorpe, Catherine

APPLICANT: Weng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

FILE REFERENCE: BBI357 US NA

CURRENT APPLICATION NUMBER: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/133038

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133437

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133428

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133436

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/137667

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Microsoft Office 97

SEQ ID NO 82

LENGTH: 164

TYPE: PRT

ORGANISM: Zea mays

US-10-078-929-82

Query Match 26.5%; Score 287; DB 12; Length 164;

Best Local Similarity 39.9%; Pred. No. 2e-17;

Matches 63; Conservative 23; Mismatches 66; Indels 6; Gaps 5;

QY 48 ACAVTAKAQQGTGSGSNATADEYLAPNOKRAAVGAPLKMNGLASAAAGTVAOOROG 107

DB 3 AAAMAAAMAAATASQN--TPQDFVNLHNRADGVGPVAMDAVRVRYQDYAA--KRAG 59

QY 108 GCAFDVAGASPYGANGWASYRA-RPAEVVALWAEGRYTHANNNTCAAGRCGTYYTVV 166

DB 60 DCRIVHSG-GPFGESIFGAGRAMSADALRSWVDEKRNHLSSNCTCDGKXGCHYTVV 118

QY 167 WNTAIVGCAQASCATG-ATITLCLYPHNGVGGSPY 203

DB 119 WRRSTRIGCARVYCADNKGVFIVCSYDPGNVNGORPE 156

RESULT 6

US-10-078-929-86

Sequence 86, Application US/10078929

Patent No. US20020152497A1

GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni

APPLICANT: Miao, Guo-Hua

APPLICANT: Falco, Saverio Carl

APPLICANT: Sakai, Hajime

APPLICANT: Famodu, Omolayo O.

APPLICANT: Odell, Joan T.

APPLICANT: Meyers, Blake

APPLICANT: Thorpe, Catherine

APPLICANT: Weng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

FILE REFERENCE: BBI357 US NA

CURRENT APPLICATION NUMBER: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/133038

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133437

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133428

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133436

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/137667

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Microsoft Office 97

SEQ ID NO 86

LENGTH: 176

TYPE: PRT

ORGANISM: Oryza sativa

US-10-078-929-86

Query Match 26.5%; Score 287; DB 12; Length 176;

Best Local Similarity 40.0%; Pred. No. 2.2e-17;

Matches 70; Conservative 22; Mismatches 71; Indels 12; Gaps 7;

QY 33 AAPPTHGARVLMPGAGAVTKAQQGTGSGSNATADEYLAPNOKRAAVGAPLKMNGL 92

DB 2 APSKVSIAVL----AVNISLMAATTTTSAQNTPODYVNLHNSARADGVGPVSMDEKV 57

QY 93 ASAAAGTVAOOROGGCAFDVAGASPYGANGWASYRA-RPAEVVALWAEGRYTHAN 150

DB 58 ASFAQSYAA--KRAGDCRLQHSQ-GPYGENIFWGSAGRAMSADAAVAVSWGCKKHVHDT 114

QY 151 NTCAGRCGTYYTVVWNTAEVGCQAQASCAT--GATITLCLYPHNGVGGSPY 203

DB 115 NTCDEGKVGCHYTVVWNRKSVRIQCANVVCANRGVFI--CNIDEPGNFGNERPE 168

RESULT 7

US-10-078-929-100

Sequence 100, Application US/10078929

Patent No. US20020152497A1

GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni

APPLICANT: Miao, Guo-Hua

APPLICANT: Falco, Saverio Carl

APPLICANT: Sakai, Hajime

APPLICANT: Famodu, Omolayo O.

APPLICANT: Odell, Joan T.

APPLICANT: Meyers, Blake

APPLICANT: Thorpe, Catherine

APPLICANT: Weng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

FILE REFERENCE: BBI357 US NA

CURRENT APPLICATION NUMBER: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

```

; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 100
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-078-929-100

```

```

Query Match      25.9%; Score 280.5; DB 12; Length 167;
Best Local Similarity 35.7%; Pred. No. 7.3e-17;
Matches 70; Conservative 26; Mismatches 61; Indels 39; Gaps 8;

```

```

QY 15 APWATCCLLATLALCAAPAPTHGAVLMPGAGAVTKAOCGSGSNATDEVLAPH 74
DB 4 SPLSLVLLALASAM-----VVVTAN-----SPQDEVDPH 35
QY 75 NQARAAGVAPLRLMNAAGLASAAGTVAAOORROGCAR----ADVGAAPYANOGMSAYRA 130
DB 36 NAARAVGVGPVWDNDNA--AYAQNYAEORR-GDCQLVHSGGQYGENITYGSGGADMTA 93
QY 131 RPAEVALMVAEGRYTHANNCA--AGROCGTYTVVWRNTAEVGAQASCATGATL-T 187
DB 94 --ADVQAVWSEKQYTDHGSNCSPADKSCLTHTYQVWRRSTALIGARVVCGGGGLFI 151
QY 188 LCLYNPHGNVQOSPY 203
DB 152 ICSYNPGENVEGVSPI 167

```

```

RESULT 8
US-10-091-135-83
; Sequence 83, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/14587-051
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-10-091-135-83

```

```

Query Match      24.6%; Score 267; DB 9; Length 136;
Best Local Similarity 44.2%; Pred. No. 8.2e-16;
Matches 61; Conservative 13; Mismatches 54; Indels 10; Gaps 5;

```

```

QY 69 EYLAPHNQAARAAVGAAPLWMNAGLASAAGTVAAOORROGCARFADVGAAPYGAN--QGWA 126

```

```

DB 6 DYLAIVNDARAQVGVGPMKMDANLASRAQNYA--NSRAGOCNLHSGA--GENLAKGGG 60
QY 127 SYARPAEVALMVAEGRYTHANNCAAGROCGTYTVVWRNTAEVGAQASC-ATGAT 185
DB 61 DFTGRAA--VOLWVSERPSEYNATQCVGKRCRRHTYQVWRRNSVRLGCGRACNNNGWA 118
QY 186 LTLCLYNPHGNVQOSPY 203
DB 119 FISCNTDPPVGNMTIGORPY 136

```

```

RESULT 9
US-10-078-929-84
; Sequence 84, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 84
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (22)
; NAME/KEY: UNSURE
; LOCATION: (50)
; NAME/KEY: UNSURE
; LOCATION: (56)
; NAME/KEY: UNSURE
; LOCATION: (59)
; NAME/KEY: UNSURE
; LOCATION: (99)
; NAME/KEY: UNSURE
; LOCATION: (121)
; NAME/KEY: UNSURE
; LOCATION: (140)
; NAME/KEY: UNSURE
; LOCATION: (150)
; NAME/KEY: UNSURE

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```

? PRIOR FILING DATE: 1999-02-25
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 7
? LENGTH: 156
? TYPE: PRT
? ORGANISM: Zea mays
US-09-840-479-7

Query Match          22.1%; Score 240; DB 10; Length 156;
Best Local Similarity 44.5%; Pred. No. 1,9e-13;
Matches 53; Conservative 16; Mismatches 44; Indels 6; Gaps 4

OY      69  EYLAPHNQARAAYGAVAPLPMNAGLSAAGAATVAGQRRGGCAFPADVGASP--YGANQGRA 126
          :: ||| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      15  DEVPHPMAAAAGVAPSPVSMDEVAAFAFASYAQ--RQGDCKLHVSGGGPHVGEINFWC 72

OY      127 SYRA-RAEYVALVAMVEGRYTHANTCAGACROCTTYQVVMRTVAEGCAQASCATGA 184
          | : : | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
DB      73  GGSWMKASDAVGLAMVEKQNYDINSNCAGAKVCGHYQVVMRRSP-SAAPASATTA 130

RESULT 14
US-10-078-929-98
? Sequence 98, Application US/10078929
? Patent No. US20020152497A1
? GENERAL INFORMATION:
? APPLICANT: Rafalski, Antoni
? APPLICANT: Miao, Guo-Hua
? APPLICANT: Falco, Saverio Carl
? APPLICANT: Sakai, Hajime
? APPLICANT: Famodu, Omolayo O.
? APPLICANT: Odell, Joan T.
? APPLICANT: Meyers, Blake
? APPLICANT: Thorpe, Catherine
? APPLICANT: Weng, Zude
? TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
? TITLE OF INVENTION: Stress Response
? FILE REFERENCE: B1357 US NA
? CURRENT FILING DATE: 2002-02-19
? PRIOR APPLICATION NUMBER: 09/566,394
? PRIOR FILING DATE: 2000-05-05
? PRIOR APPLICATION NUMBER: 60/133038
? PRIOR FILING DATE: 1999-05-07
? PRIOR APPLICATION NUMBER: 60/133042
? PRIOR FILING DATE: 1999-05-07
? PRIOR APPLICATION NUMBER: 60/133427
? PRIOR FILING DATE: 1999-05-11
? PRIOR APPLICATION NUMBER: 60/133437
? PRIOR FILING DATE: 1999-05-11
? PRIOR APPLICATION NUMBER: 60/133428
? PRIOR FILING DATE: 1999-05-11
? PRIOR APPLICATION NUMBER: 60/133438
? PRIOR FILING DATE: 1999-05-11
? PRIOR APPLICATION NUMBER: 60/133436
? PRIOR FILING DATE: 1999-05-11
? PRIOR APPLICATION NUMBER: 60/137667
? PRIOR FILING DATE: 1999-06-04
? NUMBER OF SEQ ID NOS: 208
? SOFTWARE: Microsoft Office 97
? SEQ ID NO 98
? LENGTH: 156
? TYPE: PRT
? ORGANISM: Trillium aestivum
? FEATURE:
? NAME/KEY: UNSURE
? LOCATION: (107)..(108)..(109)..(110)
? NAME/KEY: UNSURE
? LOCATION: (137)
US-10-078-929-98

Query Match          22.1%; Score 240; DB 12; Length 156;

```


GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 04:06:26 ; Search time 44.5828 Seconds
(without alignments)
4209.836 Million cell updates/sec

Title: US-09-832-320-3
Perfect score: 612
Sequence: 1 atggcgactcgcgcagcca.....agggcagagccctactag 612

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
---------------	-------	----------------	--------	----------	-------------

No matches found

Search completed: February 22, 2003, 06:08:15
Job time : 44.5828 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 14:06:16 ; Search time 1849 Seconds
(without alignments)
7865.629 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898
Sequence: 1 ctgcgcgcactcgcgcctc.....aaaaaaaaaaaaaaaa 898

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	376.6	41.9	486	10	BE512404 946070F05
2	329.4	36.7	996	12	BG343299 HVSMEG000
3	290	32.3	362	13	BM101325 BBI01325
4	207.8	23.1	681	9	AU082529 AUI082529
5	174	19.4	293	9	AU029886 AU029886
6	142.8	15.9	500	14	BQ252852 BQ252852

7	139	15.5	759	11	AY106735
8	135.8	15.1	631	13	BM337818
9	133.8	14.9	628	12	BG840355
10	133.8	14.9	663	12	BG873702
11	133.8	14.9	714	12	BG840318
12	133.8	14.9	719	13	BM350281
13	133.8	14.9	819	11	AY105799
14	132.6	14.8	539	10	AM678619
15	132.6	14.8	539	10	BE367566
16	132.6	14.8	568	10	BE367670
17	132.6	14.8	581	13	BM337258
18	132.6	14.8	582	10	BE367638
19	132.6	14.8	587	13	BM330782
20	132.6	14.8	588	10	BE597194
21	132.6	14.8	589	10	BE367550
22	132.6	14.8	593	10	AM678759
23	132.6	14.8	611	10	BE367671
24	132.6	14.8	634	10	BE600449
25	132.6	14.8	637	10	BE367243
26	132.2	14.7	564	12	BG840588
27	132.2	14.7	611	13	BM072945
28	132.2	14.7	680	13	BM078314
29	131	14.6	581	10	AM678837
30	131	14.6	588	13	BM330588
31	129.6	14.4	686	13	BM340658
32	129.4	14.4	554	10	AM746957
33	126.8	14.1	616	12	BG842842
34	126	14.0	535	13	BM318608
35	122.8	13.7	595	9	A1861282
36	119.8	13.3	548	10	BE367270
37	119.8	13.3	563	13	BM322997
38	119.8	13.3	564	10	BE367614
39	117.2	13.1	297	10	AM923743
40	117.2	13.1	550	10	AM671887
41	116	12.9	548	13	BM325875
42	116	12.9	575	13	BM326394
43	115.6	12.9	450	13	B1786368
44	114.4	12.7	438	10	BE601076
45	114.4	12.7	491	17	BH625654

ALIGNMENTS

RESULT 1
BE512404
LOCUS
DEFINITION
946070F05.y1 946 - tassal primordialium prepared by Schmidt lab zea
mays CDNA, mRNA sequence.
ACCESSION
BE512404
VERSION
BE512404.1 GI:9733652
KEYWORDS
EST.
SOURCE
Zeae mays.
ORGANISM
Zeae mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zeae.
1 (bases 1 to 486)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946070 row: F column: 05.
Location/Qualifiers
1..486
/organism="Zeae mays"

```

/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassels primordial prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="X10LR"
/Note="Organ: tassels; Vector: HybridAP; Site_1: EcoRI;
Site_2: XhoI; George Chnuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."
BASE COUNT      100 a      131 c      150 g      105 t
ORIGIN
Query Match      41.9%; Score 376.6; DB 10; Length 486;
Best Local Similarity 98.7%; Pred. No. 2.3e-40;
Matches 390; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 469 TGGCGCTGGGTGGCGGAGGGGGGCTACTACACCCAGCAACACGCGCGCGG 528
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
47 TGGCGCTGGGTGGCGGAGGGGGGCTACTACACCCAGCAACACGCGCGG 105
QY 529 GCGCGCAGTGGCGCAGTACAGCAGTGTGTGGCGCAACCGCGAGTGGGTGCG 588
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
106 GCGCGCAGTGGCGCAGTACAGCAGTGTGTGGCGCAACCGCGAGTGGGTGCG 165
QY 589 CCGAGGCGAGTGGCGCAGCGGCGCAGCTCAGCTCTGCTGTACAAACCGCAGCA 648
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
166 CCGAGGCTTTTGGCGCAGCGGCGCAGCTCAGCTCTGCTGTACAAACCGCAGCA 225
QY 649 AGGTGAGGGGCAAGGCCCTACTAGTACGTAGTACAGTACAGTACAGTACAGT 708
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
226 AGGTGAGGGGCAAGGCCCTACTAGTACGTAGTACAGTACAGTACAGTACAGT 285
QY 709 CACTGCGCGCGCGCGCGCAGCAGTACGTAGTACAGTACAGTACAGTACAGT 768
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
286 CACTGCGCGCGCGCGCGCAGCAGTACGTAGTACAGTACAGTACAGTACAGT 345
QY 769 ACGGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
346 ACGGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 405
QY 829 TGGTTGGTATACAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
406 TGGTTGGTATACAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 440
RESULT 2
BG343299          996 bp  mRNA  linear  EST 22-OCT-2001
LOCUS             BG343299
DEFINITION       HVSMEG0005F16f Hordeum vulgare pre-anthesis spike EST library
HVCNMA0008 (white to yellow anther) Hordeum vulgare cDNA clone
HVSMEG0005F16f, mRNA sequence.
ACCESSION        BG343299
VERSION          BG343299
KEYWORDS         EST.
SOURCE           Hordeum vulgare.
ORGANISM         Hordeum vulgare.
REFERENCE        1 (bases 1 to 996)
AUTHORS          Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Fritsch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
TITLE            Development of a genetically and physically anchored EST resource
JOURNAL          for barley genomics: Morex pre-anthesis spike cDNA library
COMMENT          Unpublished (2001)
                  Contact: Wing RA
                  Clemson University Genomics Institute

```

```

100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bp bases = 471
Seq primer: AATTACCTCTACTTAAAGG
High quality sequence stop: 717.
Location/Qualifiers
1. 996
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEG0005F16f"
/clone_lib="Hordeum vulgare pre-anthesis spike EST library
HVCNMA0008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/Note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spike with awns trimmed were collected at white, green and
yellow anther stages (Fenton). Total RNA was prepared from
each pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
plu were in vivo excised to give pluscript SK(-) cDNA
phagmids. These steps were performed in the TJ Close lab
(choi) at the University of California, Riverside.
Phagmids were plated and picked at the Clemson University
Genomics Institute (CUGI) (Begum, Palmer, Fritsch, Atkins
and Wing) Plasmid DNA preparations, DNA sequencing and
sequence analysis were performed at CUGI (Wing, Yu, Fritsch
, Henry, Simmons, Oates, Rambo, Main). The sequence has
been trimmed to remove vector sequence and contains a
minimum of 100 bases of phred value 20 or above. For more
details on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders
see Close TJ, Wing R, Kleinof A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gnpages/bgn/31/cover.html)"
BASE COUNT      183 a      310 c      377 g      123 t
ORIGIN
Query Match      36.7%; Score 329.4; DB 12; Length 996;
Best Local Similarity 78.3%; Pred. No. 2.1e-34;
Matches 434; Conservative 0; Mismatches 112; Indels 8; Gaps 3;
QY 131 CTTGCCACCTCTCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCTCT 190
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
128 CTTCTCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 181
QY 191 CATGCGGCGGCGCGCGCGCGCGGTGACCAAGGCGCAGCGTGGCAACCGGCGAG 250
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
182 GCCGCGCAGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
QY 251 CAACGCGAGCGCGAGCAGTACCTGTGCGCGCGCGCGCGCGCGCGCGCGT 310
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
242 GAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 301
QY 311 GCGCCCGCTGGGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 370
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
302 GCGCCCGCTGGGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
QY 371 GCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
362 GCAGAAACAGAGAGCTGCGGCTTGGGAGCATGGCGCGCGCGCGCGCGCG 421
QY 431 GCGGTGGCGAGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGT 490
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
422 GGGGTGGCGAGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGT 481

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Qy	551	GCAgTgTgTgTgGCGCAACCCGCGAGTgCGCGCGCAGGCCAGTgCGCGCCACGGG	610
Db	542	GCAGgTgTgTgTgTGGCGCGCACCGCGCGAGGTGGGTGGGCGAGGCCAGTgTGGGCTTCGGG	601
Qy	611	CGGACGGCTCAGGCTCTGCTGTAAACCGCGACGGCGAAGTGCAGGGGCCAGAGCCCCCTA	670
Db	602	GCGCAC-CTGAGCGCTCTTGCTTTTACACCCCG-ACGGGAGACGGCCAGGGCCAGAGACCTTA	659
Qy	671	CTAGCTAGCTGAGG	684
Db	660	CTAGCCCGACGGGG	673

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
BM101325	BM101325	362 bp, mRNA, linear, EST 23-jul-2002	EBP101.S0003.I13.R	EBP101	
		1 DPA, no treatment, cv Optic, EBP101			
		Hordeum vulgare cDNA clone EBP101.S0003.I13 5', mRNA sequence.			
			BM101325		
			2	GI:21944137	
			EST.		

ORGANISM
Hordium vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triliceae; Hordium.
1 (bases 1 to 362)
REFERENCE
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
Ramsay, L., Machary, G., Marshall, D.F.M. and Waugh, R.
TITLE
Development of barley transcriptome Resources
JOURNAL
Unpublished (2001)
COMMENT
On Nov 21, 2001 this sequence version replaced gi:17032393.

Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: estescr1.sari.ac.uk
 All sequence has a phred quality score of 20 or over
 Seq primer: M3 reverse.
 location/Qualifiers
 1..362

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/cultivar="Optic"
/db_xref="taxon:4513"
/clone="EBp101_S0003_113"
/clone_lib="pistill, 1 DPA, no treatment, cv Optic, EBp101"
/tissue_type="pistill"
/dev_stage="1 DPA"
/lab_host="DH10B"
/note="Vector: pSPORI1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORI1
derived from pistills dissected from developing grains (24

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Query Match	32.3%	Score 290;	DB 13;	Length 362;
Best Local Similarity	87.6%	Pred. No. 5,3e-29;		
Matches 317; Conservative	0;	Mismatches 45;	Indels 0;	Gaps 0;

Db 1 GGGCCCCGGGTGGAGCGCCGACCTGACGGCGGGCGGGCGGCGTGGACCGCGTCCAGCA 60

[illegible][illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		1 (bases 1 to 681)		
Sasaki, T. and Yamamoto, K.		Rice cDNA from panicle (2000)		
Unpublished (2000)				
Contact: Takuji Sasaki				
National Institute of Agrobiological Resources				
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki				

```

FEATURES
source
    Tel: 81-298-38-7441
    Fax: 81-298-38-7468
    Email: tssasak@eabr.affrc.go.jp, URL: http://jgyp.dna.affrc.go.jp/
    PROJECT = "RGP"
    Location/Qualifiers
        1..681
        /organism="Oryza sativa (japonica cultivar-group)"
        /cultivar="Nippombare"
        /db_xref="taxon:39947"
        /clone="E30820"

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BASE COUNT	136 a	187 c	214 g	141 t	3 others
ORIGIN					
Query Match	23.1%	Score 207.8	DB 9	length 681	
Best Local Similarity	83.5%	Pred. 0.1, 9e-18			
Matches 258; Conservative.	0	Mismatches 49	Indels 2	Gaps 2	
365 GCAGCAGCGGCGCAGAGGGGGGTGGCGCTTGCGCGAAGTGGAGGGCAGGCGCCCTAGAGGG	423				

Db	QY
19	424
GCAGGCCGGGCGAGGGCCGCCGGTTCCCGGATCAAGCGGAAGCCCTTACGGCG	CGAGCCAGGGGTTGGGCGAGCTACCGCGCGCGCCCGCGGAGTGTTGCGCGTGTGGGTGG
78	483
GCAGCCAGGGGTTGGGCGAGCTACCGCGCGCGCCCGCGGAGTGTTGCGCGTGTGGGTGG	CGAGCCAGGGGTTGGGCGAGCTACCGCGCGCGCCCGCGGAGTGTTGCGCGTGTGGGTGG
137	79
CGAGCCAGGGGTTGGGCGAGCTACCGCGCGCGCCCGCGGAGTGTTGCGCGTGTGGGTGG	CGAGCCAGGGGTTGGGCGAGCTACCGCGCGCGCCCGCGGAGTGTTGCGCGTGTGGGTGG

Q7 300 CACCCACGGCAGCACACAGGCGCGCCGCCGGGCGGCAGCGCGCGCACTACACGCAAGTGT 339
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

(GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona

University."

BASE COUNT 109 a 118 c 181 g 92 t
ORIGIN

Query Match 15.9%; Score 142.8; DB 14; Length 500;
Best Local Similarity 63.1%; Pred. No. 6.6e-10;
Matches 270; Conservative 0; Mismatches 152; Indels 6; Gaps 3;

QY 251 CAACGCGACGCGGACGAGTACTGCGCGCGCCGACACACGCGCGCGCGCGCGCGT 310
DB 51 CACAGCGCGCGCGGAGGAGTCTTGAGGCGGACACACGAGCAAGAGCCGAAGTGGCGGT 110
QY 311 GCGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 370
DB 111 GGAAGCACTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 170
QY 371 GCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 430
DB 171 GCGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 230
QY 431 GGGGTGGGC--GAGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 487
DB 231 GCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 290
QY 488 GGGGCGGAGTACACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 547
DB 291 GAAGCAATTTACGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 350
QY 548 CACGAGGTGTGTGGCGCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
DB 351 TACGAGGTGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
QY 608 GG--GCCCGACGCTGCGCTGTGTACACCGCGCGCGCGCGCGCGCGCGCGCGCGG 664
DB 411 GGAGAGGCTGAGTGTGACCATTTTCTTATGACCACTGGACACTTGGGAGAT 470
QY 665 CCCCTACT 672
DB 471 CCCATACT 478

RESULT 7
AT106735 759 bp mRNA linear HTC 25-MAY-2002
LOCUS Zea mays PC0088779 mRNA sequence.
DEFINITION Zea mays PC0088779
ACCESSION AY106735
VERSION AY106735.1 GI:21209813
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 759)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 759)
Coe,E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES
source
Location/Qualifiers
1..759
/organism="Zea mays"
/db_xref="MaizeDB:635032"
/db_xref="taxon:4577"
/clone="PC0088779"
/clone_11b="Maize Mapping Project/DuPont Consensus
Library."
/note="this sequence is part of a project of EST
assemblies resulting from the application of public

contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT 175 a 229 c 210 g 145 t
ORIGIN

Query Match 15.5%; Score 139; DB 11; Length 759;
Best Local Similarity 61.6%; Pred. No. 1.6e-09;
Matches 258; Conservative 0; Mismatches 155; Indels 6; Gaps 2;

QY 259 CGGCGAGAGTACTGCG 318
DB 152 CGCGGAGAGTACTGCG 211
QY 319 TGGGAGGAGCG 378
DB 212 TGTCTGTGGAGAGACGCGTGGCC--GCGTACCGGAGAGACTACGCGCGCGCGCGCG 268
QY 379 AGGGGAGTGGCGCTTGGCGGAGCGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 438
DB 269 GCGACTGCAAGCTGATCATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
QY 439 CGAGTACCG 498
DB 329 CGCGCGCGAGTGTGCG 388
QY 499 ACACCGACCGCAACACACG 558
DB 389 ACAGACACGACACACACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448
QY 559 TGTGGCGCAACCG 615
DB 449 TGTGGCGCGACTCCACCG 508
QY 616 CGCTACGCTTGGCTGTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 674
DB 509 TCTTCATCATCTGCGAGTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 567

RESULT 8
BM337818/c 631 bp mRNA linear EST 16-JAN-2002
LOCUS BM337818
DEFINITION MEST217-008.T3 ISUM5-RN Zea mays CDNA clone MEST217-G08 3', mRNA
sequence.
ACCESSION BM337818
VERSION BM337818.1 GI:18167978
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 631)
Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: Various stages and tissues
including seedlings treated with a variety of hormones
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
phred software,
individual bascall and confidence value were assigned using the
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>)*
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve as spacers.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
source

Source

```

1: 631
organism="Hsa_mays"
gulfivar="B73"
db_xref="tacon:4577"
clone="MEST127-G08"
clone_lib="ISOM5-RN"
tissue_type="mixed"
lab_host="DH10B"

```

BASE COUNT	123 a	176 c	184 g	148 t
------------	-------	-------	-------	-------

ORIGIN

Query Match	15.1%;	Score 135.8;	DB 13;	Length 631;
Best Local Similarity	61.1%;	Pred. No. 4.7e-09;		
Matches 256;	Conservative	0;	Mismatches 157;	Indels 6; Gaps 2

[illegible]

QY 616 CGCTCAGCTTCGCTGTACCAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCCTACTAG 674
 ||| ||||| ||||| ||| ||||| |||
 Db 246 TCTTCATCATCTGCAGCTACCAACCCGGCGGCAACGTGCTCGGCGAGAGAGCCCCCTAATAG 188

RESULT 9	LOCUS	DEFINITION	628 bp	mrna	linear	EST 29-MAY-2001
BG840355	LOCUS	MEST12-D09.T7-1	ISUM4-IN	Zea mays	cDNA clone MEST12-D09	5', mRNA
	DEFINITION	sequence.				
ACCESSION		BG840355				
VERSION		BG840355.2				
KEYWORDS		EST.				
SOURCE		Zea mays.				
ORGANISM		Zea mays				

FEATURES

source

Source

150

1630

SECRET

Lab: 401

```
/clone_11b="1SUM4-11b"
```

```
lab host="DH10B"
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3. **DNase I sensitivity** was

1/401, 1053, 1251, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329, 1331, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1347, 1349, 1351, 1353, 1355, 1357, 1359, 1361, 1363, 1365, 1367, 1369, 1371, 1373, 1375, 1377, 1379, 1381, 1383, 1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1403, 1405, 1407, 1409, 1411, 1413, 1415, 1417, 1419, 1421, 1423, 1425, 1427, 1429, 1431, 1433, 1435, 1437, 1439, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1455, 1457, 1459, 1461, 1463, 1465, 1467, 1469, 1471, 1473, 1475, 1477, 1479, 1481, 1483, 1485, 1487, 1489, 1491, 1493, 1495, 1497, 1499, 1501, 1503, 1505, 1507, 1509, 1511, 1513, 1515, 1517, 1519, 1521, 1523, 1525, 1527, 1529, 1531, 1533, 1535, 1537, 1539, 1541, 1543, 1545, 1547, 1549, 1551, 1553, 1555, 1557, 1559, 1561, 1563, 1565, 1567, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1585, 1587, 1589, 1591, 1593, 1595, 1597, 1599, 1601, 1603, 1605, 1607, 1609, 1611, 1613, 1615, 1617, 1619, 1621, 1623, 1625, 1627, 1629, 1631, 1633, 1635, 1637, 1639, 1641, 1643, 1645, 1647, 1649, 1651, 1653, 1655, 1657, 1659, 1661, 1663, 1665, 1667, 1669, 1671, 1673, 1675, 1677, 1679, 1681, 1683, 1685, 1687, 1689, 1691, 1693, 1695, 1697, 1699, 1701, 1703, 1705, 1707, 1709, 1711, 1713, 1715, 1717, 1719, 1721, 1723, 1725, 1727, 1729, 1731, 1733, 1735, 1737, 1739, 1741, 1743, 1745, 1747, 1749, 1751, 1753, 1755, 1757, 1759, 1761, 1763, 1765, 1767, 1769, 1771, 1773, 1775, 1777, 1779, 1781, 1783, 1785, 1787, 1789, 1791, 1793, 1795, 1797, 1799, 1801, 1803, 1805, 1807, 1809, 1811, 1813, 1815, 1817, 1819, 1821, 1823, 1825, 1827, 1829, 1831, 1833, 1835, 1837, 1839, 1841, 1843, 1845, 1847, 1849, 1851, 1853, 1855, 1857, 1859, 1861, 1863, 1865, 1867, 1869, 1871, 1873, 1875, 1877, 1879, 1881, 1883, 1885, 1887, 1889, 1891, 1893, 1895, 1897, 1899, 1901, 1903, 1905, 1907, 1909, 1911, 1913, 1915, 1917, 1919, 1921, 1923, 1925, 1927, 1929, 1931, 1933, 1935, 1937, 1939, 1941, 1943, 1945, 1947, 1949, 1951, 1953, 1955, 1957, 1959, 1961, 1963, 1965, 1967, 1969, 1971, 1973, 1975, 1977, 1979, 1981, 1983, 1985, 1987, 1989, 1991, 1993, 1995, 1997, 1999, 2001, 2003, 2005, 2007, 2009, 2011, 2013, 2015, 2017, 2019, 2021, 2023, 2025, 2027, 2029, 2031, 2033, 2035, 2037, 2039, 2041, 2043, 2045, 2047, 2049, 2051, 2053, 2055, 2057, 2059, 2061, 2063, 2065, 2067, 2069, 2071, 2073, 2075, 2077, 2079, 2081, 2083, 2085, 2087, 2089, 2091, 2093, 2095, 2097, 2099, 2101, 2103, 2105, 2107, 2109, 2111, 2113, 2115, 2117, 2119, 2121, 2123, 2125, 2127, 2129, 2131, 2133, 2135, 2137, 2139, 2141, 2143, 2145, 2147, 2149, 2151, 2153, 2155, 2157, 2159, 2161, 2163, 2165, 2167, 2169, 2171, 2173, 2175, 2177, 2179, 2181, 2183, 2185, 2187, 2189, 2191, 2193, 2195, 2197, 2199, 2201, 2203, 2205, 2207, 2209, 2211, 2213, 2215, 2217, 2219, 2221, 2223, 2225, 2227, 2229, 2231, 2233, 2235, 2237, 2239, 2241, 2243, 2245, 2247, 2249, 2251, 2253, 2255, 2257, 2259, 2261, 2263, 2265, 2267, 2269, 2271, 2273, 2275, 2277, 2279, 2281, 2283, 2285, 2287, 2289, 2291, 2293, 2295, 2297, 2299, 2301, 2303, 2305, 2307, 2309, 2311, 2313, 2315, 2317, 2319, 2321, 2323, 2325, 2327, 2329, 2331, 2333, 2335, 2337, 2339, 2341, 2343, 2345, 2347, 2349, 2351, 2353, 2355, 2357, 2359, 2361, 2363, 2365, 2367, 2369, 2371, 2373, 2375, 2377, 2379, 2381, 2383, 2385, 2387, 2389, 2391, 2393, 2395, 2397, 2399, 2401, 2403, 2405, 2407, 2409, 2411, 2413, 2415, 2417, 2419, 2421, 2423, 2425, 2427, 2429, 2431, 2433, 2435, 2437, 2439, 2441, 2443, 2445, 2447, 2449, 2451, 2453, 2455, 2457, 2459, 2461, 2463, 2465, 2467, 2469, 2471, 2473, 2475, 2477, 2479, 2481, 2483, 2485, 2487, 2489, 2491, 2493, 2495, 2497, 2499, 2501, 2503, 2505, 2507, 2509, 2511, 2513, 2515, 2517, 2519, 2521, 2523, 2525, 2527, 2529, 2531, 2533, 2535, 2537, 2539, 2541, 2543, 2545, 2547, 2549, 2551, 2553, 2555, 2557, 2559, 2561, 2563, 2565, 2567, 2569, 2571, 2573, 2575, 2577, 2579, 2581, 2583, 2585, 2587, 2589, 2591, 2593, 2595, 2597, 2599, 2601, 2603, 2605, 2607, 2609, 2611, 2613, 2615, 2617, 2619, 2

BASE COUNT
ORIGIN

98 a 210 c 228 g 92 f

ORIGIN

Query Match	14.9%;	Score 133.8;	DB 12;	Length 628;
Best Local Similarity	60.9%;	Pred. No. 8.6e-09;		
Matches 254;	Conservative 0;	Mismatches 157;	Indels 6;	Gaps 2.

QY	258	ACGCGCAGACGACGACTCTGGCGCGCCGCAACAAACAGGGGGCGCGGGGGGTGGGGGTGGCCCG	317
Db	106	ACGGCGGAGGACCTTCTGTAATCTGCACAAACCGCGCGCGCGGGGAGCGGTGGGGCCG	165
QY	318	CTGCGGTGGAACGCGGGGCCCTGCGTTTGGCGCGCGCGGGGAGCGAGTGGCGGCACACACGGCGG	377
Db	166	GTGCGCTGGGAGACCCGACGGGGGCGCAGAGTACGGCGACGACGACGCGGCCAACCGCGCGCG	226
QY	378	CAGGCGGAGTGCCTGTTTGGGGGACGTGGGGGCGAGGCCCTTACGCGCGCAACACAGGGGTGG	437

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Db 226 GACTGCGGCTGTGTCACCTGGGCGCCGTTTGGGAGAACATC--TTCTGGGGCTTG 282
QY 438 GCGAGCTACCGCGCGCCGCCGCGAGGTGTGGCTGTGGGTGGCGAGGGCGGTAC 497
Db 283 GCGGGGGGGGGGCTGTGAGACGGCGCCGAGCGCTCGGTGTGGTGTGACGAGAAGAGAAC 342
QY 498 TACACCCAGCCCAACAACACACGTGCGCGGGGCGGCACTGCGGCACGTACACGACGTG 557
Db 343 TACACCTGAGCAGACACACCTGCGACCCCGGCAAGTGTGGGGCCACTACACGACAGTGT 402
QY 558 GTGTGGCGCAACACCGCCGAGGTGGGTGGCGGCGAGCCAGCTGGGCGC---CACGGGCGCG 614
Db 403 GTGTGGCGCAAGTGTACACCCGATCGGTGCGCGCGCTGTGTGCGCGACACACCGCGGCG 462
QY 615 ACAGCTACGCTGTGCTGTGTACAAACCGCAGCGCAACGTCAGAGGCGGACCCCTTAC 671
Db 463 GTCTTCATGCTGTGACACTGTACGACCCCGCGGCAACGTCACAGCGGCGGCGCCGTTG 519

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RESULT 10

BG873702/c

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LOCUS MEST9-A05.t3 ISUM4-TN Zea mays cDNA clone MEST9-A05 3', mRNA
DEFINITION sequence.
ACCESSION BG873702
VERSION BG873702.1 GI:14245120
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 663)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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/clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/label="DH10B"
/label="Vector: pT733PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AACTGAGAGATTCGGCGCGGAGAGATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol. catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT733PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

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BASE COUNT

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113 a 218 c 197 g 135 t

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Query Match 14.9%; Score 133.8; DB 12; Length 663;
Best Local Similarity 60.9%; Pred.No. 8.3e-09;
Matches 254; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

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QY 258 ACAGCGGACGACGATCTGTGGGCGGCGACAAACAGGCGCGCGCGGTGGCGTGGCCCG 317
Db 658 ACAGCGGACGACGATCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 599
QY 318 CTGGGCGGAGAACCGGCGCGCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 377
Db 598 GTGGCGGAGGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539
QY 378 CAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 437
Db 538 GACTGCGGCTGTGTGCACTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 482
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QY 498 TACACCCAGCCCAACAACACGTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 557
Db 421 TACACCTGAGCAGCAACACCTGCGACCCCGGCAAGTGTGGGCGGCGGCGGCGGCGGCGG 362
QY 558 GTGTGGCGCAACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 614
Db 361 GTGTGGCGCAAGTGTACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 302
QY 615 ACAGCTACGCTGTGCTGTGTACAAACCGCAGCGCAACGTCAGAGGCGGACCCCTTAC 671
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RESULT 11

BG840318

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LOCUS MEST9-A05.t7-1 ISUM4-TN Zea mays cDNA clone MEST9-A05 5', mRNA
DEFINITION sequence.
ACCESSION BG840318
VERSION BG840318.1 GI:14206640
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 714)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA CTA TAG).
Location/Qualifiers
1..714
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="MEST9-A05"
/clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/label="DH10B"
/label="Vector: pT733PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand

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FEATURES

source

Individual basecall and confidence value were assigned using the phred software, <http://depts.washington.edu/ventures/collabtr/direct/index.htm#html>. Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.ligc.org/soflab/>). PCR parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.

PCR Primers
 FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

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/organism="Zea mays"
/cultivar="B73"
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/tissue_type="mixed"
/lab host="DH10B"
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/note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seedling (1, 2, 8, 11 DAG).

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Mixed mature tissues (11, 21, 38, 69, 11 DAG), kernels (3, 5, 10, 15, 20, 25, 30, 30 DAG), Adventitious roots (65 DAG)

), tassels (3-35 cm, 25 and 30 DAG), immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated

Cycloheximide-treated callus, Anaerobic treated seedlings

Kinetin-treated seedlings, ACPC

Brassinolide-treated seedlings, ABA (Abscissic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings

seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was

prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'

resulting DNA:RNA hybrid was treated with RNase H and used

used as a template for DNA for catalyzed second strand synthesis. After the addition of EcoRI adaptors, the

resulting molecules were directionally cloned into the

then went through one round of normalization to CoT value

Research 6: 791-806, 1996)."

Similarity	60.9%; Pred. No. 8e-09;
Length	19;
DB	13;
Score	133.8;
Length	14.9%;

2; waps 0; index 0; mismatches 0; conservative 0; 2;

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540

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CGGGGGGGCGTGGAGCCGCCGACGCGCTGCGGTCTGGGTGGACGAGAGAGGAAC 423

[illegible]


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ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEX: (202) 887-0763
FAX: 706141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-440-856A-9

Query Match      8.2%; Score 73.8; DB 1; Length 1288;
Best Local Similarity 38.3%; Pred. No. 4.6e-05;
Matches 192; Conservative 66; Mismatches 238; Indels 5; Gaps 14

QY 125 CTTGCTCCTCGGCACCCCTTCCTGGCCGTGCGGCCCGCCGCGGCGCACACCAGCGCGCGG 184
DB 108 CCTAGCGCCMGATATMGTATGCTCTGSGCGCTGSACTTCSRYCYSWSMYWMSMASSG 167
QY 185 CGTCTCATGCGGGCGGCGCGCGCGCGGTGACCAAGGCGACAGAG-----GTGGCACC 239
DB 168 CACCAAGCCSKYCATTGCKCGCCSTFKCMCCACGSCGTGGAGCCGAACGCAAMBSGCGMS 227
QY 240 GGCACGGGAGCAAGCGGACGCGGACGACAGTACTTGCGCGCCGACCAACAGGCGCGCGG 299
DB 228 CCCAACWCSSATGCCCCAAAGAGGCTGSAAGGGAAGGTGGCCATTGTACSGGCGGSGCGMS 287
QY 300 GCGGTGGGCGTGGCCCGCTGCGGTGGAACGCGGCGCTGCGTTCGGCGCGCGCGGAGG 359
DB 288 GGGATCGGSGAGGCGSATGTGTMGGCTGTTCGYAAGCAACGCGGCGCMRGRTGTATCGCG 347
QY 360 GTGGCGAGCAGACGCGCGGACGAGGCGGCGGTGCGGCTTTCGCGAGCTGGGGGCGACGCCCTAC 419
DB 348 GACATCGACGACGCGCGCGGSGAGGCGCTGGCGKCGCGCTGGGSCCGCASGTCRGTTC 407
QY 420 GCGCGCAACCAAGGGGTGGGCGAGCTACCGCGGCGCGCGCGCGAGGTGTGGCGCTGGG 479
DB 408 GTGCGSTCGACAGCTGTCGTGGAGSASACGTSNKGCGCGCGTGSACTGSOGCGYTSG 467
QY 480 GTGGCGAGGCGGCTACTACACCCACGCAACACAGCTGCGCGCGCGGCGGCGGCTGCG 539
DB 468 CGCSHYGRCGSGGSCGTGACGTSYWTSYGCAACAACGCGCGGGGTGTGGGCGCCAGACG 527
QY 540 GGCACTGACGAGCAAGTGTGTGGCGCAACACCGCGGAGTTCGGTGGCGGACGCGCACG 599
DB 528 CGCGCGGCGCAAGACATCTGTCTTCGACCGCGSSGAGTTGACCGCGTCTCGCGCTC 587
QY 600 TCGCGCACGCGGCGCGCACGCTC 620
DB 588 AACGGCGTGGGCGCGCGGCTC 608

RESULT 5
US-07-945-283-1
Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
NUMBER OF SEQUENCES: Involving The EP0 and LIT Genes
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
STATE: IL
```

```

1  COUNTRY: USA
2  ZIP: 61604
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC-DOS/MS-DOS
7  SOFTWARE: PatentIn Release #1.0, Version #1.25
8  CURRENT APPLICATION DATA:
9  APPLICATION NUMBER: US/07/945,283
10 FILING DATE: 19920911
11 CLASSIFICATION: 424
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Ribando, Curtis P
14 REGISTRATION NUMBER: 27976
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 309-685-4011 ext.513
17 TELEFAX: 309-685-4128
18 INFORMATION FOR SEQ ID NO: 1:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 8438 base pairs
21 TYPE: NUCLEIC ACID
22 STRANDEDNESS: double
23 TOPOLOGY: linear
24 MOLECULE TYPE: DNA (genomic)
25 ANTI-SENSE: NO
26 ORIGINAL SOURCE:
27 ORGANISM: Pseudorabies virus
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: 622..6495
31 FEATURE:
32 NAME/KEY: variation
33 LOCATION: replace(1099, "g")
34 FEATURE:
35 NAME/KEY: variation
36 LOCATION: replace(1267, "t")
37 FEATURE:
38 NAME/KEY: variation
39 LOCATION: replace(1381, "c")
40 FEATURE:
41 NAME/KEY: variation
42 LOCATION: replace(1566, "c")
43 FEATURE:
44 NAME/KEY: variation
45 LOCATION: replace(7010, "g")
46 US-07-945-283-1
47
48 Query Match 7.8%; Score 70.4; DB 1; Length 8438;
49 Best Local Similarity 49.8%; Pred. No. 0.00022;
50 Matches 26; Conservative 0; Mismatches 256; Indels 8; Gaps 3.
51
52 QY 88 ACCTCCTCTGCTGCCCGCGCCCATGCGACGCGTGCCTTCCTTCGACCACTCTCTG 147
53 Db 3978 AGCGGCGCTTGCCGCCCGGCGCCCGGTCCTCTGTCGTCGCGGTGCGCCGCGTCCG 4037
54
55 QY 148 CGCTGCGCGCGCGCGCGCGCGCGAGCCACCGCGCGCGCGCTGCTCTATATCCCGGCGCGG 207
56 Db 4038 CGCGGAGGCGCGGAGCGCGGAGG---AGCCCTTGCTCTCTGCGCGTCCCGGCGGCGG 4093
57
58 QY 208 GCGCGGTGACCAAGCGCGACGAGGGTG-GCACCGGACGCGGACGACGACGAGCGGAGAC 266
59 Db 4094 GCGCGGCGCGCGCGCGGCGCTTCTTCTTGCGCGCTCGGGCGGTGGGTCGCGGCGGCGG 4153
60
61 QY 267 GATTACTTGGCGCGGACACACAGGCGCGCGCGCGGTGGGCGTGGCGCCGCTGCGGTGG 326
62 Db 4154 GGGGACCTGACGTAGCGCGGAGGAGCGGAGAGGCGGACTTGGTGGCGGAGCTGGACTTG 4213
63
64 QY 327 AACGCGGCGCTGCTTCGCGCGCGCGCGGAGCGGTGCGGACGACGCGCGCGAGGCGGG 386
65 Db 4214 GTGCTGTGAGCCGAGACTGTGGTGTGGCGGCGGCGGTGAGGAGGCCCGGAGAGCGCGGAG 4273
66
67 Y 387 TGGCGCTTGGCGGAGCTGGGGGCGACGCCCTTAGCGCGCGAACCAGGAGGTGGCGAGCTAC 446

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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-181-271A-11

Query Match 7.2%; Score 65; DB 1; Length 696;
Best Local Similarity 56.2%; Pred. NO. 0.0015;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCGAGGTGGTGGCGGTGGCGGCGGCGGTACTACACCCAGCCCAACAA 516
DB 319 CCGCTAAGCCCTGCAGATGGTGCATATGAGAAACAGTATTATGCCCAACCTCA 378
QY 517 CGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576
DB 379 CTTGTGCCCAAGAGAGAGGTGTGTGACACTATACCTAGTGTGGGTACGCTG 438
QY 577 AGCTGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
DB 439 GTGTGGATGTGTGTGAGGTTCAGTGTACAAATGAGCATATATGTCTTGCAACTATG 498
QY 637 ACCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673
DB 499 ATCTCCAGTATGTATATAGGCAAAAGCCATACTA 535

RESULT 8
US-08-449-315-11
Sequence 11, Application US/08449315
Patent No. 5650505

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.

APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689

```

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-449-315-11

Query Match
Best Local Similarity 56.2%; Pred. No. 0.0015; Length 696;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCCGAGGTGTGGCTGTGGGTGGCGGAGGGGGGCTACACCCGCAACACA 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 CCGGTAAAGCGGTGAGATGTGGTCAATGAGAAACAGTATTATGCCACGACTCAACA 378

QY 517 CGTGGCGCGGGGGCGGCACTGGCGACGTACACGACGAGTGTGTGGCCACACCGCG 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 CTGTGGCCCAAGACAGGTGTGTGACACTATCTCAGGTGGTGGCTAACTCGGTTC 438

QY 577 AGGTGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GTGTGGATGTGCTAGGGTTCACTGTAACATGAGAGATATATGCTCTTGCACTATG 498

QY 637 ACCCGACGCGCACTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673
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Db 499 ATCCTCAGGTAAATGTTATAGGCAAAAGCCCATACTA 535

RESULT 9
US-08-444-803-11
; Sequence 11, Application US/08444803
; Patent No. 5654414
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Speerison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 base pairs
; STRANDEDNESS: single
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-444-803-11

Query Match
Best Local Similarity 56.2%; Pred. No. 0.0015; Length 696;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCCGAGGTGTGGCTGTGGGTGGCGGAGGGGGGCTACTACCCGCAACACA 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 CCGGTAAAGCGGTGAGATGTGGTCAATGAGAAACAGTATTATGCCACGACTCAACA 378

QY 517 CGTGGCGCGGGGGCGGCACTGGCGACGTACACGACGAGTGTGTGGCCACACCGCG 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 CTGTGGCCCAAGACAGGTGTGTGACACTATCTCAGGTGGTGGCTAACTCGGTTC 438

QY 577 AGGTGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GTGTGGATGTGCTAGGGTTCACTGTAACATGAGAGATATATGCTCTTGCACTATG 498
```

QY 637 ACCCGACGACGTCGACGGCCAGACCCCTACTA 673
| | | | | | | | | | | | | | | | | | | | | |
DB 499 ATCTCCAGGTATGTATTAGCAAAAGCCACTACTA 535

RESULT 10
US-08-449-043-11

; Sequence 11, Application US/08449043
; Patent No. 5689044

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: Williams, Sherice C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-449-043-11

Query Match 7.2%; Score 65; DB 1; Length 696;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCCGAGTGTGGGCGGTGGGTGGCGGAGGCGCGGTACTACACCCGCAACACACA 516
| | | | | | | | | | | | | | | | | | | | | |
DB 319 CCCTTAAGCGCGTCGAGATGGGTCAATAGAAACAGTATTATGCGCCAGCTCAAAACA 378
QY 517 CGTGCAGCGGCGGCGCGCAGTGGCGGACGACGAGTGGTGGCGCAACACCGCGC 576
| | | | | | | | | | | | | | | | | | | | | |
DB 379 CTGTGCCCAAGACAGAGGTGTGGACACTATACAGTGGTGGTGGCTACTGCGTTC 438
QY 577 AGTGGGTTGCGCGCAGCCAGCTGCGCCAGCGGCGCGCCACGCTCAGCGTCTGCTGTACA 636
| | | | | | | | | | | | | | | | | | | | | |
DB 439 GTCTTGATGTGCTAGGTTCACTATACAAATGAGATATATGTTCTCTGCAACTATAG 498
QY 637 ACCCGACGACGTCGACGGCCAGACCCCTACTA 673
| | | | | | | | | | | | | | | | | | | | | |
DB 499 ATCTCCAGGTATGTATTAGCAAAAGCCACTACTA 535

RESULT 11

US-08-456-265A-11
; Sequence 11, Application US/08456265A
; Patent No. 5767369

GENERAL INFORMATION:

APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Goodman, Robert M.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA

```

1  ZIP: 10591
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  SOFTWARE: Patentin Release #1.0, Version #1.25
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/456,265A
9  FILING DATE: 31-MAY-95
10 CLASSIFICATION: 435
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/181,271
13 FILING DATE: 13-JAN-1994
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/093,301
16 FILING DATE: 16-JUL-1993
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 07/937,197
19 FILING DATE: 6-NOV-1992
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 07/678,378
22 FILING DATE: 1-APR-1991
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 07/305,566
25 FILING DATE: 6-FEB-1989
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/165,667
28 FILING DATE: 8-MAR-1988
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 08/042,847
31 FILING DATE: 6-APR-1993
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 07/632,441
34 FILING DATE: 21-DEC-1990
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 07/425,504
37 FILING DATE: 20-OCT 1989
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 07/848,506
40 FILING DATE: 6-MAR-1992
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: US 07/768,122
43 FILING DATE: 27-SEP-1991
44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: US 07/580,431
46 FILING DATE: 7-SEP-1990
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: US 07/368,672
49 FILING DATE: 20-JUN-1989
50 PRIOR APPLICATION DATA:
51 APPLICATION NUMBER: US 07/329,018
52 FILING DATE: 24-MAR-1989
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: US 08/045,957
55 FILING DATE: 12-APR-1993
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Weigs, J. Timothy
58 REGISTRATION NUMBER: 38,241
59 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (919)541-8587
62 TELEFAX: (919)541-8689
63 INFORMATION FOR SEQ ID NO: 11:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 696 base pairs
66 TYPE: nucleic acid
67 STRANDEDNESS: single
68 TOPOLOGY: linear
69 MOLECULE TYPE: cDNA
70 US-08-456-265A-11
71
72 Query Match 7.28; Score 65; DB 1; Length 696
73 Best Local Similarity 56.28; Pred. No. 0.0015;

```

```

Matches 11, Conservative 0; Mismatches 95; Indels 0; Gaps 0;
OY 457 CCGCCAGGTGTGTGGCGCTGTGTGGTGTGGCGGAGGGCGGTACTAACCCAGCCCAACAA 516
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 CCGGTAAAGGCCCTCGAGATGTGGGTCAATGAAACACGTATTATTAAGCCCAAGCTCA 378
OY 517 CGTGGCGCGGGGGGGCGGACGTGGGGACGTATACGACGAGTGTGTGGCGGACACCGCG 576
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 CTGTGGCCCAAGACACAGTGTGTGGACACTATACACTCAAGTGTGTTGGCGTAACTCG 438
OY 577 AGGTGGGTGCGGCGGACCGACGTGGCGCCAGCGGCCACCGCTCAGCCTGTGCTGTACA 636
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GTGTGTATGTGCTAGAGGTTCAETGTACAAATAGAGGATATATGTCTTTCGAACATAG 498
OY 637 ACCGCAAGCAACGTGCAGGCGGCAAGCCCTACTA 673
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 499 ATCCCGAGTAAATTATATAGCAAAAGCCCATACTA 535

RESULT 12
US-08-455-416-11
; Sequence 11, Application US/08455416
; Patent No. 5777200
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesling, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Sherioka C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,416
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566

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; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/C/GC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-455-416-11

Query Match          7.2%   Score 65; DB 1; Length 696;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY      457 CCGCCGAGGTGGTGGCGCTGTGGTGTCGCCGAGGGGGGCTACTACACCACGCCAACAACA 516
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       319 CCGCTAGAGCGCGTCGAGATGTGGGTCAATGAAGAACAAGTATTATGCCAGACTCAACA 378

QY      517 CGTGCAGCGGGGGGGCGGACAGTGGCGCACGTACACGACAGGTGTGGGGGCAACGCGCCG 576
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       379 CTGTGCCCACGAGCACAGGTGTGGACACTATACGACAGGTGGTTGGGTAACTCGGTTTC 438

QY      577 AGGTTCGGGTGCGGACGCGACGCTGCGCACGCGGCGCCACGCTCACGCTCTGCTGTACA 636
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       439 GTGTGGATGTGCTAGAGGTTCACTGTACAAATGAGAGATATATGTCTCTTGCAACTATG 498

QY      637 ACCGCGACGCGAACGTGCACAGGCGCCAGAGCCCTACTA 673
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       499 ATCTCCAGGTAAATGTTATAGGCAAAAAGCCCATCTA 535

RESULT 13
US-08-455-244-11
; Sequence 11, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
```

APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Melns, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Unes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,244
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672

CITY: Hawthorne

Query Match 7.28; Score 65; DB 1; Length 696;

Db	181	CCGCGTCTCTATGCGGGGCGCGCGCGCGCTATACCAAGGCGAGCGAGGTGGCACGG	240
Qy	241	GCAGCGGAGCAACGCGCAAGCGGAGCAAGTACTGGCGCCGACAAACCAAGCGCGCGG	300
Db	241	GCAGCGGAGCAACGCGCGAGCGCGGACAGTACTGGCGCGCCGACAAACCAAGCGCGCGG	300
Qy	301	CGGTGGGCGTGGCCCCCGTGGGCGGGAACCGCGGGCCCTGGCTTCGGCGGCGCGGGGAGCG	360
Db	301	CGGTGGGCGTGGCCCCCGTGGGCGGGAACCGCGGGCCCTGGCTTCGGCGGCGCGGGGAGCG	360
Qy	361	TGGCGCAGCAGCGGCGCGGAGCGGCGGCGGCGGCGGTCGTCGGAGCGTGGGGGCGACCCCTACG	420
Db	361	TGGCGCAGCAGCGGCGCGGAGCGGCGGCGGCGGTCGTCGGAGCGTGGGGGCGACCCCTACG	420
Qy	421	GGCGGACCAACGAGGGGTGGGCGAGCTACCGCGCGCGCGCCCGCGAGGTGGTGGCGCTGTGGG	480
Db	421	GGCGGACCAACGAGGGGTGGGCGAGCTACCGCGCGCGCGCCCGCGAGGTGGTGGCGCTGTGGG	480
Qy	481	TGGCGGAGGGGCGGATACACACCCAGCCGCAACACGTCGCGCGCGGAGCGGCGAGTGGG	540
Db	481	TGGCGGAGGGGCGGATACACACCCAGCCGCAACACGTCGCGCGCGGAGCGGCGAGTGGG	540
Qy	541	GCACGTACACGCGAGGTGGTGGGCGCAACACCGCGAGGTGGGTCGCGGCGAGCGAGCT	600
Db	541	GCACGTACACGCGAGGTGGTGGGCGCAACACCGCGAGGTGGGTCGCGGCGAGCGAGCT	600
Qy	601	GGCGCCACGAGGGCGCCACGCTACGCTCTGCTGTATCAACCCCGAGCGCAACGTGCAGGGGCC	660
Db	601	GGCGCCACGAGGGCGCCACGCTACGCTCTGCTGTATCAACCCCGAGCGCAACGTGCAGGGGCC	660
Qy	661	AGAGCCCTACCTAGCTACGTAGGTTCATCAGGTCGTATAGGAGGAGGACCACTGGCGCGG	720
Db	661	AGAGCCCTACCTAGCTACGTAGGTTCATCAGGTCGTATAGGAGGAGGACCACTGGCGCGG	720
Qy	721	CCGGGCGGACGCGGAGTACGTAGGTTCATCAGTCTTCTCTAGTTGGTCAACGAAAGGCTG	780
Db	721	CCGGGCGGACGCGGAGTACGTAGGTTCATCAGTCTTCTCTAGTTGGTCAACGAAAGGCTG	780
Qy	781	TTTTGGTGATATCCGGGAGGTTGTCGTTGGTGTGATCACTGTTGGTTGGTGTGA	840
Db	781	TTTTGGTGATATCCGGGAGGTTGTCGTTGGTGTGATCACTGTTGGTTGGTGTGA	840
Qy	841	TCAGCTTTTGTCCGGGTAAAAA	898
Db	841	TCAGCTTTTGTCCGGGTAAAAA	898
RESULT 2			
US-09-832-320-3			
Sequence 3, Application US/09832320			
Patent No. US20010049834A1			
GENERAL INFORMATION:			
APPLICANT: Crane, Edmund H.			
APPLICANT: Crane, Virginia C.			
TITLE OF INVENTION: Maize Pathogenesis-Related			
FILE REFERENCE: 35718/214291			
CURRENT APPLICATION NUMBER: US/09/832,320			
CURRENT FILING DATE: 2001-04-10			
PRIOR APPLICATION NUMBER: US 60/195,801			
PRIOR FILING DATE: 2000-04-10			
NUMBER OF SEQ ID NOS: 3			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 3			
LENGTH: 612			
TYPE: DNA			
ORGANISM: Zea mays			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)...(612)			
US-09-832-320-3			

Query Match	68.2%;	Score 612;	DB 10;	Length 612;
Best Local Similarity	100.0%;	Pred. No. 3.7e-101;		
Matches 612;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	63	ATGGGCGACTGCGGCAAGCAACCAACATCTCTCTGCTCCCGGCGCCATATGGCAAGGGG	122
Db	1	ATGGGCGACTGCGGCAAGCAACCAACATCTCTCTCTCCCGGCGCCATATGGCAAGGGG	60
QY	123	TGCTTGCTCTCGGCAACCCCTCTCTCGGGCTCTGCGGCGCGCGCGGCGGCAACCGCGGG	182
Db	61	TGCTTGCTCTCTCGGCAACCCCTCTCTCGGGCTCTGCGGCGCGCGCGGCGGCAACCGCGGG	120
QY	183	CGGTCCTCATGCGGGCGCGCGGGCGCGGTCATCCAAAGCGCAGCAAGGATGGACACGGC	242
Db	121	CGGTCCTCATGCGGGCGCGCGGGCGCGGTCATCCAAAGCGCAGCAAGGATGGACACGGC	180
QY	243	AGCGGCAAGCAACCGGAGGGGCGAGATCTTGCGCGCGGCACAAACCAAGGCGCGCGGGG	302
Db	181	AGCGGCAAGCAACCGGAGGGGCGAGATCTTGCGCGCGGCACAAACCAAGGCGCGCGGGG	240
QY	303	GTGGGCGCTGGCCCCGCGTGGTGGAAACGCGGGGCTTGCTTGCGCGCGCGCGGGGACGGTG	362
Db	241	GTGGGCGCTGGCCCCGCGTGGTGGAAACGCGGGGCTTGCTTGCGCGCGCGCGGGGACGGTG	300
QY	363	GCGGAGCAGGGGCGCGGCGAGGGCGGGTGGGGCTTGCGGCAAGTGGGGGCGAAGCCCTTACGGC	422
Db	301	GCGGAGCAGGGGCGCGGCGAGGGCGGGTGGGGCTTGCGGCAAGTGGGGGCGAAGCCCTTACGGC	360
QY	423	GCGAACCAGGGGGTGGGCGAGCTACCGCGCGCGCCCGCGAGGTGGTGGCGCTGTGGGTG	482
Db	361	GCGAACCAGGGGGTGGGCGAGCTACCGCGCGCGCCCGCGAGGTGGTGGCGCTGTGGGTG	420
QY	483	GCGAAGGGGCGGTACTACACCAAGCCAAACAAACAGTGCACCAGCGGCGCGAGTCCGGC	542
Db	421	GCGAAGGGGCGGTACTACACCAAGCCAAACAAACAGTGCACCAGCGGCGCGAGTCCGGC	480
QY	543	ACGTACACAGCAGGTGTGTGTGGCGCAACACCGCGAGGTGCGGGTGGCGGAGGCGCACTGC	602
Db	481	ACGTACACAGCAGGTGTGTGTGGCGCAACACCGCGAGGTGCGGGTGGCGGAGGCGCACTGC	540
QY	603	GCCACGCGGCGCGACGCTACACCTTGGCTGTACAAACCGCAGCGCAACGTCAGGGCCAG	662
Db	541	GCCACGCGGCGCGACGCTACACCTTGGCTGTACAAACCGCAGCGCAACGTCAGGGCCAG	600
QY	663	AGCCCTACTAG 674	
Db	601	AGCCCTACTAG 612	

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RESULT 3
US-09-840-479-12
; Sequence 12, Application US/09840479
; Patent No. US20010025380A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/840,479
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/257,583
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 12
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)..(583)
US-09-840-479-12

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Best Local Similarity	61.68;	Pred. No. 1.3e-16;
Matches 258;	Conservative	0; Mismatches 155; Indels 6; Gaps 2;

QY	259	CGCGGACAGAGTACCTGGGCGCCGCAACACAGCGCGCGCGGTGGGCGTGGCCCGC	31
Db	168	CGCGGACAGAGTACCTGGGCGCCGCAACACAGCGCGCGCGGTGGGCGTGGCCCGC	22
QY	319	TGCGGTGGAACGGGGGCGCTGGGCTTGGGCGGCGCGGGGACGAGTGGCGCAAGCGCGCGC	37
Db	228	TGTCCTTGGAGACGACACCGTCCG---GGCTACGGCGAGACCTACGGCGCGCAAGCGCGC	28
QY	379	AGGGCGGGTCCGCGTTCCGCGGACGTTGGGGGCGACCGCCCTACGGCGCGCAACCAAGGGTGGG	43
Db	285	GGCGACTGCCAGCTGATCCACTCCGCGGGGGCCCTACGGCGGAAGACCTTCTTGGGGTCCG	34
QY	439	CGAGCTACCGCGCGCGCGCCCGCGGACGTTGGTGGCTGTGGTGGCGGAGGGCGGTACT	49
Db	345	CGCGGCGCGAGTGGTGGGCGTCCGACGCGCGCGTCTCTGGTGGTCCGGAAGACGATCT	40
QY	499	ACACCCAGCCCAACAAACAGTCCGCGCGGGGGCGGACGTGGCGGCAAGTACAGCAAGTGG	55
Db	405	ACGACGACGACACCAACAGCTGGCGGAGGGGCGACAGTGTCCGCGCACTACAGCAAGTGG	46
QY	559	TGTGGCGCAACACCGCGGAGGTTGGGGTCCGCGACGAGCAAGTCCG---CCAGGGGCGCA	61
Db	465	TGTGGGCGCACTCCACCGCGATCGGTGTGGCCCGTCTGTCTGCAACCAAGCGCGGGG	52
QY	616	CGCTCACGCTCTGGCTGTACCAACCGCGCAAGCGCAACGTGACAGGGCCAGAGCCCTTACTAG	674
Db	525	TCTTTCATCTGCGAGCTACACCGCGCGGCGGCAAGTGTGTCGCGAGAGCCCTTACTAG	583

Accession	Sequence	Position
Dp	325 GGGGGGGCAGCGCCCTGGGAAGGCGCTCGAACGCCCTTCGGCTTGTGGGTGGGGAGACAGCAGA	354
Qy	496 ACTACACCCACGCGCAACACAGTCGGCGCGGGGGGGCAGTGGCGACGCTACACGCAGG	555
Dp	385 ACTAGATTATCAACAGCAAGCTGCGGGGGGGGAAGTGTGGCGCACTACACGCAG	444
Qy	556 TGGTGTGGCGGAACACCGCGCGAGTGGGTGGCGGAGCCAGTGTGGCGCCACGGGC---G	612
Dp	445 TCGTGTGGCGCAA-TTCCCCCGCATTCGGCTGGCGCCGCTGCTTGACAAACGGGGGTG	503
Qy	613 CCACGCTACGCTGTGCTGTATACACCGCAGCAGCTGACAGGGCGAGGCCCTACT	672
Dp	504 GGGTCTTCATCATCCGTGCAGACTACAAACCGCGCGGCACTTCCGGGSAACAGACCTACT	553
Qy	673 AGCTTAGCT 680	
Dp	564 AGCTACTT 571	

	15.3%;	Score 137.6;	DB 10;	Length 866;
Query Match	Best Local Similarity 62.4%;	Pred. No. 2,4e-16;	Mismatches 267;	Conservative 0; Mismatches 154; Indels 7; Gaps 3;
QY	259	CGCGGACGATGACTCTGGCGCCGCAACAACGAGCGCGCGCGGCGTGGGGTGGCCCGC	318	
Db	145	CGCGGAGGACTTCGTGAACCGCGCAATATGGCGCGCGCGCGTGTGGCGTGGCGCGG	204	
QY	319	TGCGGTGAACCGCGGCGCTTGCTTGCGCGCGCGCGGAGCGGTGGCGCACACGCGCGCG	378	
Db	205	TGTCGTGGGATGAAACGTTGGCGCGCTTCGCGGAGACTACGCCGCGCACGAGCGG	264	
QY	379	AGGGCGGGTGGCGCTTCCGCGACGCGGGGGCGACCCCTTACGCGCGAACGAGGTGGG	438	
Db	265	ACTCGAACTGTGTGCACTTCGCGCGCGCGGCCCAACCACTACGGGAGAAATCTTTGGG	324	
QY	439	CGAGCTACCGCGC---GCGCCCGCGGAGGTGTGTGGCGCTTGGGTGGCGAGGAGCGGT	495	

Query Match	13.6%	Score 121.8	DB 12	Length 783
Best Local Similarity	60.6%	Pred. No. 1.6e-13		
Matches 254	Conservative	0	Mismatches 157	Indels 8
				Gaps
258	ACGGCGGAGGAT	TACTTGGCCCGCCACACACAGGCGCGCGCGGTGGCGGTGCCCCG	317	

Db 566 TACTAGCAACT 577

RESULT 8
US-10-078-929-85
; Sequence 85, Application US/10078929
; Patent No. US20020152497A1

GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
Stress Response

FILE REFERENCE: B01357 US NA

CURRENT APPLICATION NUMBER: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/133038

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133437

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133428

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133438

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133436

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/137667

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Microsoft Office 97

SEQ ID NO 85

LENGTH: 714

TYPE: DNA

ORGANISM: Oryza sativa

US-10-078-929-85

Query Match 13.1%; Score 117.4; DB 12; Length 714;
Best Local Similarity 55.4%; Pred. No. 9.4e-13;

Matches 270; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Db 188 CCTATCGCGGCGCGCGCGGTGACCAAGCGGAGGCTGGACCGGACGCG 247

Db 39 CCTCGCCCGCTGCTCGCGCGGTGACCTGCTGCGCGCGGTGACCGCGG 98

Db 248 CAGCAACGCGGCGGCGGAGTACCTGCGCGCGGTGACCGCGGCGGCGG 307

Db 99 GCGCGAGAACGCGCGGCGGAGTACCTGCGCGCGGTGACCGCGGCGGCGG 158

Db 308 CGTGCGCGCGGTGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367

Db 159 CGTGCGCGCGGTGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 218

Db 368 GCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427

Db 219 GCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 275

Db 428 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487

Db 276 CTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 335

Db 488 GCGCGCGGTACTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTA 547

Db 336 GAAGAGAACTACACTACGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGTA 395

Db 548 CACGCGGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607

Db 396 CACCGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 455

Db 608 G---GGCGCGCGGTACCGCTGCGCGGTACCAACCGCGCGCGCGCGCGCGG 664

Db 456 GAACCGCGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 515

Db 665 CCCGTAC 71

Db 516 CCCGTTC 522

RESULT 9

US-10-078-929-99

; Sequence 99, Application US/10078929

; Patent No. US20020152497A1

GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
Stress Response

FILE REFERENCE: B01357 US NA

CURRENT APPLICATION NUMBER: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/133038

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133437

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133428

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133438

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133436

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/137667

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Microsoft Office 97

SEQ ID NO 99

LENGTH: 604

TYPE: DNA

ORGANISM: Triticum aestivum

US-10-078-929-99

Query Match 12.1%; Score 108.6; DB 12; Length 604;
Best Local Similarity 56.9%; Pred. No. 3.4e-11;

Matches 242; Conservative 0; Mismatches 174; Indels 9; Gaps 2;

Db 259 CCGCGGAGGAGTACTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 318

Db 82 CGCGCGGAGGAGTCTGCGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 141

Db 319 TCGCGGTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 378

Db 142 TGACCTGGGAGCAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 201

Query Match	8.0%;	Score 72.2;	DB 9;	Length 492
Best Local Similarity	50.6%;	Pred. No. 0.00011;		

[illegible]

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Run on:      March 18, 2003, 10:55:25 ; Search time 272 Seconds
              (without alignments)
              7434.906 Million cell updates/sec
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Title: US-09-832-320-1
Perfect score: 898
Sequence: 1 ctgcgcgcactgcagctc.....aaaaaaaaaaaaaaaa 898
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 200000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

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2:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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22:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	898	100.0	898	24	ABA96417	
2	612	68.2	612	24	ABA96418	Maize PR1-C10 encod
3	140.6	15.7	731	16	AAQ95804	Maize PR1-C10 codo
4	139	15.5	749	20	AAZ21207	PR-1 like gene PR
5	137.6	15.3	866	20	AAZ21191	zea mays pathogene
6	121.8	13.6	806	20	AAZ21194	zea mays pathogene
7	105	11.7	846	24	ABL50008	zea mays pathogene
8	85.2	9.5	679	21	AAC43084	Nucleotide Sequenc
9	83.6	9.3	683	21	AAC37078	Arabidopsis thalia

C	10	83.4	9.3	114955	20	AA53491	Human adenosine A1
C	11	81.6	9.1	114955	20	AA53491	Human adenosine A1
C	12	72.2	8.0	779	21	AA47173	Arabidopsis thaliana
C	13	71.2	7.9	664	24	ABL59002	Nicototid sequenc
C	14	70.4	7.8	8438	15	ABQ73500	DNA encoding pseud
C	15	70	7.8	712	24	ABQ40858	oligonucleotide for
C	16	70	7.8	712	24	ABQ40859	oligonucleotide for
C	17	69.8	7.8	65140	22	AD117184	Streptomyces nours
C	18	69.8	7.8	125401	22	AD117186	Streptomyces nours
C	19	69.6	7.8	3198	20	AAQ2974	Human II-1ra BAC C
C	20	69	7.7	1983	22	AA545413	Fructan exohydrola
C	21	68	7.6	679	24	AB559001	Nicototid sequenc
C	22	67.8	7.6	12561	22	AAH26500	Rabbit low density
C	23	67.6	7.5	117213	19	AAH62176	HSV-2 strain SB5 C
C	24	67.6	7.5	154746	24	AD25519	Human herpesvirus
C	25	66.4	7.4	881	24	ABQ29954	Oligonucleotide for
C	26	66.4	7.4	881	24	ABQ29955	Oligonucleotide for
C	27	66.2	7.4	1281	13	AAQ23396	HSV-1 (MGH-10) tCp
C	28	66.2	7.4	2561	22	AAH26500	Rabbit low density
C	29	66	7.3	27541	22	AD117185	Streptomyces nours
C	30	65.8	7.3	25360	22	AAH8314	S. spindosa DNA fra
C	31	65.8	7.3	29738	22	AAH8317	S. spindosa DNA fra
C	32	65.2	7.3	3957	22	AAQ09686	HSV-2 immediate ea
C	33	65.2	7.3	154746	24	AD25519	Human herpesvirus
C	34	65	7.2	696	11	AAQ06182	PR-1c cDNA cloned
C	35	65	7.2	696	20	AAV2807	Tobacco PR-1c gene
C	36	65	7.2	666	20	AAV72899	PR-1c protein enco
C	37	65	7.2	721	10	AAH91021	Nicototiana tabacum
C	38	65	7.2	24379	18	AAH93095	Streptomyces fremo
C	39	65	7.2	24379	19	AAV25925	Streptomyces roseo
C	40	65	7.2	27541	22	AD117185	Streptomyces nours
C	41	65	7.2	125401	22	AD117186	Streptomyces nours
C	42	64.6	7.2	4653	22	AAH30931	Maize P-glycoprote
C	43	64.6	7.2	8036	22	AAH30930	Maize P-glycoprote
C	44	64.4	7.2	4257	19	AAH68520	The nucleotide seq
C	45	64.4	7.2	4257	19	AAH68520	Infected cell prot

ALIGNMENTS

XX	RESULT 1
XX	ABA96417
ID	ABA96417 standard; CDNA; 898 BP.
XX	
AC	ABA96417;
XX	
DT	02-APR-2002 (first entry)
XX	
DE	Maize PRL-C10 encoding CDNA SEQ ID NO 1.
XX	
KW	Maize; pathogen-related; PRL-C10; plant; transgenic; gene; ss
XX	
OS	Zea mays.
XX	
FH	Key
FT	CD5
FT	Location/Qualifiers
FT	63..674
FT	/*tag= a
XX	/product= "PRL-C10"
PN	US2001049834-A1.
XX	
PD	06-DEC-2001.
XX	
PF	10-APR-2001; 2001US-0832320.
XX	
PR	10-APR-2000; 2000US-195801P.
XX	
PA	(CRAN/) CRANE E H.
PA	(CRAN/) CRANE V C.
XX	
PI	Crane EH, Crane VC;
XX	


```
XX PD 02-SEP-1999.
XX PF 11-FEB-1999; 99WO-US03011.
XX PR 26-FEB-1998; 98US-0076100.
XX PR 27-MAR-1998; 98US-0079648.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Crane VC;
XX DR WPI; 1999-527621/44.
XX DR P-PSDB; AAY29944.
XX PT New promoter sequences from pathogenesis-related genes of maize
XX PS Example 3; Page 72-73; 86pp; English.
XX CC AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters
XX CC isolated from a family of maize (Zea mays) genes encoding pathogenesis
XX CC related (PR-1) proteins. The promoters are useful for expressing
XX CC heterologous genes (including genes for disease resistance) in plants,
XX CC especially dicots, or monocots i.e. maize. The promoters are useful for
XX CC the genetic manipulation of plants to exhibit specific phenotypes,
XX CC particularly enhanced resistance to pathogen-caused disease. Pathogens
XX CC include viruses such as tobacco or cucumber mosaic virus, ringspot
XX CC virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,
XX CC insects, nematodes and fungi. The present sequence encodes a maize
XX CC PR-1 protein given in the present invention.
XX SQ Sequence 749 BP; 160 A; 235 C; 206 G; 148 T; 0 other;

Query Match 15.5%; Score 139; DB 20; Length 749;
Best Local Similarity 61.6%; Pred. No. 1.8e-12;
Matches 258; Conservative 0; Mismatches 155; Indels 6; Gaps 2;

OY 259 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 318
DB 168 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 227
OY 319 TGGGTGGAACGGGGGCTTGGCGCGCGCGCGGAGCGTGGCGCGCGCGCGC 378
DB 228 TGTCTGGGAGCAGCGCGTGGCGCGCGCGCGGAGCGTGGCGCGCGCGCGC 284
OY 379 AGGCGGAGTGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 438
DB 285 GCGACTGCGACGTGATCCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 344
OY 439 CGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 498
DB 345 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 404
OY 499 ACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 558
DB 405 ACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 464
OY 559 TGTGGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 615
DB 465 TGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 524
OY 616 CGGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 674
DB 525 TCTTCATCATCTGACGTACACCGCGCGCGCGCGCGCGCGCGCGCGCGC 583

RESULT 5
AAZ21191
ID AAZ21191 standard; DNA; 866 BP.
XX AC AAZ21191;
XX DT 22-NOV-1999 (first entry)
```

```
XX DE Zea mays pathogenesis-related class I PR-1#52 gene.
XX KW Zea mays; maize; pathogenesis-related class I; PR-1; promoter;
XX KW regulation; expression; disease resistance; genetic manipulation;
XX KW tobacco mosaic virus; cucumber mosaic virus; ringspot virus;
XX KW necrosis virus; maize dwarf virus; viroid; bacterial; insect;
XX KW nematode; fungal; ss.
XX OS Zea mays.
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 111..581
XX FT /*tag= a
XX FT /*product= "PR-1#52"
XX FT /*note= "pathogenesis-related class I protein"
XX PN W09943819-A1.
XX PD 02-SEP-1999.
XX PF 11-FEB-1999; 99WO-US03011.
XX PR 26-FEB-1998; 98US-0076100.
XX PR 27-MAR-1998; 98US-0079648.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Crane VC;
XX DR WPI; 1999-527621/44.
XX DR P-PSDB; AAY29944.
XX PT New promoter sequences from pathogenesis-related genes of maize
XX PS Claim 22; Page 65-66; 86pp; English.
XX CC AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters
XX CC isolated from a family of maize (Zea mays) genes encoding pathogenesis
XX CC related (PR-1) proteins. The promoters are useful for expressing
XX CC heterologous genes (including genes for disease resistance) in plants,
XX CC especially dicots, or monocots i.e. maize. The promoters are useful for
XX CC the genetic manipulation of plants to exhibit specific phenotypes,
XX CC particularly enhanced resistance to pathogen-caused disease. Pathogens
XX CC include viruses such as tobacco or cucumber mosaic virus, ringspot
XX CC virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,
XX CC insects, nematodes and fungi. The present sequence encodes a maize
XX CC PR-1 protein given in the present invention.
XX SQ Sequence 866 BP; 213 A; 228 C; 240 G; 185 T; 0 other;

Query Match 15.3%; Score 137.6; DB 20; Length 866;
Best Local Similarity 62.4%; Pred. No. 3e-12;
Matches 267; Conservative 0; Mismatches 154; Indels 7; Gaps 3;

OY 259 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGCGGTGGCGTGGCCCGC 318
DB 145 CGCGGAGCAGTACTGTGGCGCCGACACAGCGCGCGCGCGCGCGCGCGCGC 204
OY 319 TGGGTGGAACGGGGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 378
DB 205 TGTCTGGGAGTGAACGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 264
OY 379 AGGCGGAGTGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 438
DB 265 ACTGCAACGTGTGTCACATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 324
OY 439 CGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 495
DB 325 GCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 384
OY 496 ACTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 555
```

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DB 385 ACTAGATTACAAACGCAACGCTGCGGCGGGAGGTGTGCGGCACCTACACGCAAG 444
OY 556 TGGTGTGGCGCAACACCGCGAGTGGGTGCGCGCAGCGCACTGCGGACGGCG--G 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 445 TGGTGTGGCGCAAC-ATCCCGGCATCGGTGCGCGCGGTCTGTGCAACACGCGGTG 503
OY 613 CCACGCTACGCTGTGCTGTACAAACCGCACGCGACGTGCGAGGCGCAAGCCCTACT 672
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 504 GCGTCTTCATCACTGCAACTACACCGCGCGCACTCCGCGACAGAGACCTACT 563
OY 673 AGTAGCT 680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 564 AGCTACT 571

RESULT 6
AAZ21194
ID AAZ21194 standard; DNA; 806 BP.
AC AAZ21194;
DT 22-NOV-1999 (first entry)
DE Zea mays pathogenesis-related class I PR-1#93 gene.
XX
XX Zea mays; maize; pathogenesis-related class I; PR-1; promoter;
KM regulation; expression; disease resistance; genetic manipulation;
KM tobacco mosaic virus; cucumber mosaic virus; ringspot virus;
KM necrosis virus; maize dwarf virus; viroid; bacterial; insect;
KM nematode; fungal; ss.
XX
XX Zea mays.
OS
FH
FH
FT CDS Location/Qualifiers
FT 42..686
FT /*tag= a
FT /product= "PR-1#93"
FT /note= "pathogenesis-related class I protein"
FT
FT
XX W09943819-A1.
XX
XX 02-SEP-1999.
XX
XX 11-FEB-1999; 99WO-US03011.
XX
XX 26-FEB-1998; 98US-0076100.
XX
XX 27-MAR-1998; 98US-0079648.
XX
XX (PRON-) PIONEER HI-BRED INT INC.
XX
XX Crane VC;
PI
XX WPI; 1999-527621/44.
XX
XX P-PSDB; AAY29943.
XX
XX New promoter sequences from pathogenesis-related genes of maize
XX
XX Claim 22; Page 74-75; 86pp; English.
XX
XX AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters
XX isolated from a family of maize (Zea mays) genes encoding pathogenesis
XX related (PR-1) proteins. The promoters are useful for expressing
XX heterologous genes (including genes for disease resistance) in plants,
XX especially dicots, or monocots i.e. maize. The promoters are useful for
XX the genetic manipulation of plants to exhibit specific phenotypes,
XX particularly enhanced resistance to pathogen-caused disease. Pathogens
XX include viruses such as tobacco or cucumber mosaic virus, ringspot
XX virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,
XX insects, nematodes and fungi. The present sequence encodes a maize
XX PR-1 protein given in the present invention.
XX
XX Sequence 806 BP; 158 A; 243 C; 260 G; 144 T; 1 other;
XX
XX

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Query Match 13.6%; Score 121.8; DB 20; Length 806;
Best Local Similarity 60.6%; Pred. No. 6.6e-10;
Matches 254; Conservative 0; Mismatches 157; Indels 8; Gaps 3;

OY 258 ACGGCGGACGAGTACCTGCGCGCCGACACMACAGCGCGCGGTGGGCTGGGCCG 317
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DB 141 ACGCGGAGAGACTTCGTGATCTGCACACACCGCGCGCGCGGACGCGCTGGGCCG 200
OY 318 CTGGGTGTGAACGCGGCGCTTGCTTGGCGCGCGGCGGAGCGTGGCGACGCGCGG 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 GTGGCGTGGGAGACGACGAGGTGGCGAGGTACGCGGACTACCGCGGAAGCGCGCG 260
OY 378 CAGGCGGCGGTGCGGCTTGGCGGACGTGGGGCGGCGAGGCCCTACGCGCGGAGCG 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 261 GACTGCCGCGCTGTGCACTGTGGG--GGGCGTTGGCGAGACATCTTGTGGGCTCG 317
OY 438 GCGAGTACCGCGCGCGCCCGCGAGGTGGTGGCGCTGTGGGTGCGGAGGGCGGTAC 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 GCGGGCGGCGCGTGGAGCGCGCGGACGCGCGCTCGGTCGTGGTGGACGAGAGAGAAC 377
OY 498 TACACCGACCGCAACACACAGTGGCGCGGCGGCGGCGAGTGGCGACGTACACGAGT 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 TACCACCTGAGCAGACACCTGTGACCCCGGCAAGGTGTGGCGCCTACACGAGTGT 437
OY 558 GTGTGGCGCA--ACACCGCGAGGTGGGCGCGCGAGGCGACCTGCGC--CACGGGG 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 GTGTGGGCGCAGGTGTGCACCCGATGGCTGGCGCGCGCTGTGCGCGACACCGCG 497
OY 613 CCACGCTACGCTGTGCTGTACACCCGACGCGACGCAAGTGCAGGCGCAGAGCCCTAC 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 498 GCGTCTTCATCGTCTGACGTACGACCCCGGCGCAACGTCAACGCGCAGCGCGTTTC 556

RESULT 7
ABLS9008
ID ABL59008 standard; DNA; 846 BP.
AC ABL59008;
DT 20-AUG-2002 (first entry)
DE Nucleotide sequence of an antibacterial protein.
XX
XX Antibacterial protein; microbe resistance; plant; gene; ss.
XX
XX Elaeis guineensis.
OS
FH
FH
FT CDS Location/Qualifiers
FT 35..523
FT /*tag= a
FT /product= "antibacterial protein"
FT
FT
XX JP2002095477-A.
XX
XX 02-APR-2002.
XX
XX 20-SEP-2000; 2000JP-0285905.
XX
XX 20-SEP-2000; 2000JP-0285905.
XX
XX PA (MITU ) MITSUBISHI CHEM CORP.
XX
XX PA (BADA-) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.
XX
XX PA (PAKR-) PT PAKRIE BROS.
XX
XX PA (BIOI-) BIOINDUSTRI KYOKAI SH.
XX
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
XX
XX WPI; 2002-439987/47.
XX
XX P-PSDB; ABB77767.
XX
XX New protein and its gene, useful for creating plants with high
XX resistance to pathogenic microbes -
XX
XX Claim 3; Page 8-9; 13pp; Japanese.
XX
XX

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PR	06-APR-1999;	99US-012827234
PR	08-APR-1999;	99US-01282714
PR	16-APR-1999;	99US-01282844
PR	21-APR-1999;	99US-01300077
PR	23-APR-1999;	99US-01300449
PR	23-APR-1999;	99US-01300510
PR	28-APR-1999;	99US-01300891
PR	30-APR-1999;	99US-01314440
PR	30-APR-1999;	99US-01324048
PR	04-MAY-1999;	99US-01324481
PR	11-MAY-1999;	99US-01342816
PR	14-MAY-1999;	99US-01344219
PR	14-MAY-1999;	99US-01348229
PR	14-MAY-1999;	99US-01343370
PR	18-MAY-1999;	99US-01347468
PR	18-MAY-1999;	99US-01349441
PR	20-MAY-1999;	99US-01351244
PR	21-MAY-1999;	99US-01353353
PR	24-MAY-1999;	99US-01356299
PR	25-MAY-1999;	99US-01360211
PR	27-MAY-1999;	99US-01363592
PR	28-MAY-1999;	99US-01367882
PR	01-JUN-1999;	99US-01372222
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PR	04-JUN-1999;	99US-01375502
PR	07-JUN-1999;	99US-01377244
PR	08-JUN-1999;	99US-01380094
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PR	21-JUN-1999;	99US-01398177
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PR	30-JUN-1999;	99US-01409831
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PR	01-JUL-1999;	99US-01418442
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PR	02-JUL-1999;	99US-01422055
PR	06-JUL-1999;	99US-01423290
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PR	09-JUL-1999;	99US-01429200
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PR	13-JUL-1999;	99US-01435342
PR	14-JUL-1999;	99US-01435344
PR	15-JUL-1999;	99US-01440085
PR	16-JUL-1999;	99US-01440805
PR	16-JUL-1999;	99US-01443425
PR	19-JUL-1999;	99US-01444331

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16099.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 27-AUG-1999; 99US-0151080.

KW	hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis,
KW	prostate cancer; ss.
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PA (UYEC-) UNIV EAST CAROLINA.

NYC@ JW;

WPI; 1999-229400/19.

New antisense oligonucleotide

Page 37: 130mm.

The specification describes

CC directed against at least 2
CC non-coding regions of RNAs

initiation codons, genomic
5'-end, the 3'-end and the

or more diseases, conditions, regions and all segments of

oligonucleotides (specificity)

conditions are those associ-

inflammation, allergic rhin

pulmonary hypertension, pul

CC Lymphomas, carcinomas e.g.

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Best Local Similarity 34.28;

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